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OM protein - protein search, using sw model

Run on: August 12, 2003, 15:28:01 ; Search time 84 Seconds

(Without alignments)
591.445 Million cell updates/sec

Title: US-09-807-132-4

Perfect score: 1611
Sequence: 1 MDSLNGRVRTEFVFLGLTDN.....VKSAMKQARQRFVFTSYT 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1611	100.0	313	21	AA190872
2	1611	100.0	313	22	AAU10306
3	1611	100.0	313	22	AA190872
4	1611	100.0	313	22	AA190872
5	1380	85.7	327	22	AA190872
6	992	61.6	330	22	AA190872
7	985	61.1	335	22	AA190872
8	938	58.2	311	22	AAU24670
9	938	58.2	311	22	AA190872

10	938	58.2	311	23	ABP95716	Human GPCR polypep
11	938	58.2	311	23	ABP95716	Human GPCR polypep
12	938	58.2	311	23	AAU95650	Human olfactory an
13	938	58.2	311	23	AAU95650	G-coupled olfactory
14	929	57.7	314	22	AA190872	Human olfactory re
15	929	57.7	314	22	ABP95834	Human GPCR polypep
16	929	57.7	314	23	ABJ04000	Human G-protein co
17	929	57.7	314	23	ABJ04001	Human G-protein co
18	929	57.7	314	23	ABJ04035	Human G-protein co
19	929	57.7	314	23	AAU85337	G-coupled olfactory
20	929	57.7	314	24	ABU11200	Human G-protein co
21	927.5	57.6	310	22	AAU24739	Human olfactory re
22	927.5	57.6	310	22	AAU24739	Human olfactory re
23	927.5	57.6	310	23	ABP95708	Human GPCR polypep
24	927.5	57.6	310	23	ABG76839	Human G-protein co
25	927.5	57.6	310	23	AAU95651	Human olfactory an
26	927.5	57.6	310	23	AAU85339	G-coupled olfactory
27	927.5	57.6	310	24	ABU11155	Human G-protein co
28	927.5	57.6	313	22	AAU24739	Human olfactory re
29	927.5	57.6	314	22	AAU24739	Human olfactory re
30	919	57.0	322	22	AAU24739	Human olfactory re
31	919	57.0	324	23	ABP61145	Human GPCR polypep
32	919	57.0	324	23	AAU95659	Human olfactory an
33	919	57.0	348	22	AAU24739	Human olfactory re
34	919	57.0	348	23	ABP95924	Human GPCR polypep
35	919	57.0	348	23	AAU85340	G-coupled olfactory
36	917.5	57.0	310	23	ABP51597	Human G-protein co
37	911	56.5	325	24	ABU11173	Human G-protein co
38	905	56.2	315	23	AAU24739	Human olfactory re
39	905	56.2	315	23	AAU24739	Human G-protein co
40	905	56.2	325	22	AAU24739	Human olfactory re
41	905	56.2	325	23	ABP95833	Human GPCR polypep
42	905	56.2	325	23	AAU85338	G-coupled olfactory
43	900	55.9	318	22	AAU05130	Human olfactory re
44	900	55.9	318	22	AAU05130	Human olfactory re
45	900	55.9	318	23	AAU95525	Human olfactory an

ALIGNMENTS

RESULT 1
AA190872
ID AA190872 standard; Protein: 313 AA.
XX
AC AA190872;
XX
DT 29-AUG-2000 (first entry)
XX
AC Human G protein-coupled receptor GPCR14-1 SEQ ID NO:4.
DE Human, G protein-coupled receptor; GPCR; olfactory receptor; OR;
KW Immune response; haematopoiesis; immunomodulatory; regulation.
XX
OS Homo sapiens.
XX
PN WO200021999-A1.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-JP05578.
XX
PR 09-OCT-1998; 98JP-0288565.
PR 07-DEC-1998; 98JP-0347546.
PR 21-DEC-1998; 98JP-0363537.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Maeda M, Nakata Y, Nomura H;
XX
FI WPI: 2000-317946/27.
DR N-PSDB; AAA38953.
XX

PT Novel G-protein-coupled receptor proteins encoded by the olfactory
 PR receptor gene family are useful in screening drugs or their ligands to
 PT regulate the control of the immune response and hematopoiesis -
 XX
 PS Claim 1; Page 100-102; 159pp; Japanese.

XX The present sequence represents a G-protein-coupled receptor protein
 CC designated G14-1, isolated from human, which is functional in the
 CC immune response and control of hematopoiesis. The G-protein-coupled
 CC receptors from the present invention have immunomodulatory and
 CC hematopoiesis regulatory activities. The G-protein-coupled receptors
 CC and nucleotide sequences encoding them can be used in screening drugs
 CC or their ligands to regulate the functions of immune response and
 CC hematopoiesis control.

XX Sequence 313 AA;

Query Match 100.0%; Score 1611; DB 21; Length 313;
 Best Local Similarity 100.0%; Pred. No. 4,4e-172;
 Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSLNQTRVTEFVFGITDNRVLEMLFPMASAIYMLTSGNLIITIAVTPPSLHTPMY 60
 DB 1 MDSLNQTRVTEFVFGITDNRVLEMLFPMASAIYMLTSGNLIITIAVTPPSLHTPMY 60
 QY 61 FFLSNLSFIDICHSSVTPKMLEGLLEKRTISFQNCITQFLPHLFCACIFLLIIVAY 120
 DB 61 FFLSNLSFIDICHSSVTPKMLEGLLEKRTISFQNCITQFLPHLFCACIFLLIIVAY 120
 QY 121 DRYVAICTPLHYPNNMNRVCIOLVFALMLGTVHSLGQTFILIRLPYCGNIIIDSYFCD 180
 DB 121 DRYVAICTPLHYPNNMNRVCIOLVFALMLGTVHSLGQTFILIRLPYCGNIIIDSYFCD 180
 QY 121 DRYVAICTPLHYPNNMNRVCIOLVFALMLGTVHSLGQTFILIRLPYCGNIIIDSYFCD 180
 DB 121 DRYVAICTPLHYPNNMNRVCIOLVFALMLGTVHSLGQTFILIRLPYCGNIIIDSYFCD 180
 QY 181 VPLVIKACTDLYTLGILIVTNSGTSISCFPLAVTSMYVILVSLRKHSABGRQALSTC 240
 DB 181 VPLVIKACTDLYTLGILIVTNSGTSISCFPLAVTSMYVILVSLRKHSABGRQALSTC 240
 QY 241 SAHFVVALFPGPCIFITRBDTSISIDKVSVFYTVTPILNPIYTLRNEEVSAMQ 300
 DB 241 SAHFVVALFPGPCIFITRBDTSISIDKVSVFYTVTPILNPIYTLRNEEVSAMQ 300
 QY 301 LRQOVFFTKSYT 313
 DB 301 LRQOVFFTKSYT 313

RESULT 2

AAU10306 standard; protein; 313 AA.

AAU10306;

25-JAN-2002 (first entry)

G-protein coupled receptor (GCREC) #7.

KM G-protein coupled receptor; GCREC; vaccine; gene therapy;
 KM cell proliferation disorder; cancer; arteriosclerosis;
 KM neurological disorder; epilepsy; stroke; cardiovascular disorder;
 KM hypertension; ischemic heart disease; gastrointestinal disorder;
 KM anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
 KM diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
 KM schizophrenia disorder; neuroskeletal disorder.

OS Homo sapiens.

PN WO200166742-A2.

PD 13-SEP-2001.

PF 01-MAR-2001; 2001WO-US06814.

PR 03-MAR-2000; 2000US-186854P.

PR 10-MAR-2000; 2000US-186834P.
 PR 17-MAR-2000; 2000US-190453P.
 PR 20-MAR-2000; 2000US-190730P.

XX (INCY-) INCYTE GENOMICS INC.

XX Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;
 PI Lu DM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J;
 PI Harland L, Walsh RT, Lo TP, Borowsky ML;

DR WPI; 2001-65676/75.

DR N-PSDB; AAS15903.

PT Novel G-protein coupled receptor polypeptides, for treating and
 PT preventing autoimmune/inflammatory disorders, neurological disorders,
 PT cell proliferative disorders, cardiovascular disorders and viral
 PT infections -

Claim 1; Page 119; 141pp; English.

The invention describes a novel isolated polypeptide, selected from a
 group of 21 G-protein coupled receptor polypeptides (GCREC) and useful in
 vaccines and gene therapy. The polypeptide (I) is useful for screening
 CC for agonist or antagonist of (I), compounds specifically binding to (I),
 CC or compounds that modulate the activity of (I). The polynucleotide
 CC encoding (I) is useful for screening a compound for effectiveness in
 CC altering expression of a target polynucleotide comprising (II), by
 CC exposing a sample comprising the target polynucleotide to a compound,
 CC detecting altered expression of the target polynucleotide, and comparing
 CC the expression of the target polynucleotide in the presence of varying
 CC amounts of compound and in the absence of the compound. (I) and (II) are
 CC useful for diagnosis, treatment and prevention of cell proliferative
 CC disorders (e.g. cancer, arteriosclerosis, atherosclerosis), neurological
 CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
 CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,
 CC ischemic heart disease), gastrointestinal disorders (e.g. anorexia,
 CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
 CC osteoporosis, psoriasis), and metabolic disorders such as obesity.
 CC Furthermore, the polynucleotide is useful as primers for detecting
 CC single nucleotide polymorphisms; as elements in microarray, to monitor or
 CC measure protein-protein interactions, drug-target interactions, and gene
 CC expression profiles; to generate a transcript image of a tissue or cell
 CC type, and to generate hybridization probes useful in mapping the
 CC CC naturally occurring genomic sequence. This is the G-protein coupled
 CC receptor 7 (GCREC-7), one of 21 GCREC proteins described in the method of
 CC the invention.

XX Sequence 313 AA;

Query Match 100.0%; Score 1611; DB 22; Length 313;
 Best Local Similarity 100.0%; Pred. No. 4,4e-172;
 Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSLNQTRVTEFVFGITDNRVLEMLFPMASAIYMLTSGNLIITIAVTPPSLHTPMY 60
 DB 1 MDSLNQTRVTEFVFGITDNRVLEMLFPMASAIYMLTSGNLIITIAVTPPSLHTPMY 60
 QY 61 FFLSNLSFIDICHSSVTPKMLEGLLEKRTISFQNCITQFLPHLFCACIFLLIIVAY 120
 DB 61 FFLSNLSFIDICHSSVTPKMLEGLLEKRTISFQNCITQFLPHLFCACIFLLIIVAY 120
 QY 121 DRYVAICTPLHYPNNMNRVCIOLVFALMLGTVHSLGQTFILIRLPYCGNIIIDSYFCD 180
 DB 121 DRYVAICTPLHYPNNMNRVCIOLVFALMLGTVHSLGQTFILIRLPYCGNIIIDSYFCD 180
 QY 121 DRYVAICTPLHYPNNMNRVCIOLVFALMLGTVHSLGQTFILIRLPYCGNIIIDSYFCD 180
 DB 121 DRYVAICTPLHYPNNMNRVCIOLVFALMLGTVHSLGQTFILIRLPYCGNIIIDSYFCD 180
 QY 181 VPLVIKACTDLYTLGILIVTNSGTSISCFPLAVTSMYVILVSLRKHSABGRQALSTC 240
 DB 181 VPLVIKACTDLYTLGILIVTNSGTSISCFPLAVTSMYVILVSLRKHSABGRQALSTC 240
 QY 241 SAHFVVALFPGPCIFITRBDTSISIDKVSVFYTVTPILNPIYTLRNEEVSAMQ 300
 DB 241 SAHFVVALFPGPCIFITRBDTSISIDKVSVFYTVTPILNPIYTLRNEEVSAMQ 300


```

Db      1 MDSLNGRTVTEVFVGLIDNRVLEMLFMAFSAIYMLTISGNILIIATVFTPSLTPMY 60
QY      61 FFLSNLSFIDICHSSVTPPKMLEGLLEKRTISFDNCITQLPFLHLPACAEIFLLITVAY 120
Cc      61 FFLSNLSFIDICHSSVTPPKMLEGLLEKRTISFDNCITQLPFLHLPACAEIFLLITVAY 120
Db      61 FFLSNLSFIDICHSSVTPPKMLEGLLEKRTISFDNCITQLPFLHLPACAEIFLLITVAY 120
QY      121 DRYVAICTPLHYPNVNMNRVCIOLVFALMLGTVHSLGQTFLLIRLPYCGPNIIDSYPCD 180
Db      121 DRYVAICTPLHYPNVNMNRVCIOLVFALMLGTVHSLGQTFLLIRLPYCGPNIIDSYPCD 180
QY      181 VPLVTKACTDPTLYLGLIIVNSGTSLSGCLAVVTSYVVLVSLRKHSAGRRQKALSTC 240
Db      181 VPLVTKACTDPTLYLGLIIVNSGTSLSGCLAVVTSYVVLVSLRKHSAGRRQKALSTC 240
QY      241 SAHFVWVALFPGPCIFITRPTDPSFSDIKVSVFYVTVPPLNPFITYTLRNEEVSAMQ 300
Db      241 SAHFVWVALFPGPCIFITRPTDPSFSDIKVSVFYVTVPPLNPFITYTLRNEEVSAMQ 300
QY      301 LRQRCVFETKSYT 313
Db      301 LRQRCVFETKSYT 313

```

RESULT 5

AAG72705 standard; Protein; 327 AA.

AAG72705;

31-JUL-2001 (first entry)

Murine OR-like polypeptide query sequence, SEQ ID NO: 2387.

Mouse; olfactory receptor; OR; primary scent determination;
secondary scent determination; polypeptide library; odour receptor;
scent profile; scent fingerprint; scent representation.

Mus musculus.

MO200127158-A2.

19-APR-2001.

06-OCT-2000; 2000WO-US27582.

08-OCT-1999; 99US-0158615.

24-FEB-2000; 2000US-0184809.

(DIGI-) DIGISCENTS.

(YEDA) YEDA RES & DEV CO LTD.

Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

WPI; 2001-290713/30.

New polynucleotides which encode polypeptides involved in olfactory
sensation for identifying olfactory agonists and antagonists -

Example 6; Page 1618-1619; 1857pp; English.

The present sequence is a polypeptide encoded by one of 105 newly mined
mouse genes. It was used as a query sequence in a database search of
olfactory receptor (OR)-like sequences. The invention relates to isolated
polynucleotides encoding polypeptides involved in olfactory sensation.
The polynucleotides can be used in screening for olfactory agonists and
antagonists. The methods allow for the determination of primary scents
and the identification of the odour receptors used to detect these
primary scents. The methods also enable determination of secondary scents
and the identification of combinations of odour receptors that are
involved in detecting such secondary scents. This enables the
construction of a scent representation (also called a scent fingerprint
or scent profile), which may be used to re-create and edit scents.
Libraries of olfactory receptors are useful for determining the

CC interaction pattern of a composition with the receptors, and can be
used for determining differences in the olfactory faculties of different
individuals.

CC Sequence 327 AA;

Query Match 85.7%; Score 1380; DB 22; Length 327;
Best Local Similarity 85.6%; Pred. No. 4e-146;
Matches 262; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

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QY      1 MDSLNGRTVTEVFVGLIDNRVLEMLFMAFSAIYMLTISGNILIIATVFTPSLTPMY 60
Cc      1 MDSLNGRTVTEVFVGLIDNRVLEMLFMAFSAIYMLTISGNILIIATVFTPSLTPMY 60
Db      3 MGNALQVTEVFIFVGLIDNRVLEMLFMAFSAIYMLTISGNILIIATVFTPSLTPMY 62
QY      61 FFLSNLSFIDICHSSVTPPKMLEGLLEKRTISFDNCITQLPFLHLPACAEIFLLITVAY 120
Cc      61 FFLSNLSFIDICHSSVTPPKMLEGLLEKRTISFDNCITQLPFLHLPACAEIFLLITVAY 122
Db      63 FFLSNLSFIDICHSSVTPPKMLEGLLEKRTISFDNCITQLPFLHLPACAEIFLLITVAY 122
QY      121 DRYVAICTPLHYPNVNMNRVCIOLVFALMLGTVHSLGQTFLLIRLPYCGPNIIDSYPCD 180
Cc      121 DRYVAICTPLHYPNVNMNRVCIOLVFALMLGTVHSLGQTFLLIRLPYCGPNIIDSYPCD 180
Db      123 DRYVAICTPLHYPNVNMNRVCIOLVFALMLGTVHSLGQTFLLIRLPYCGPNIIDSYPCD 182
QY      181 VPLVTKACTDPTLYLGLIIVNSGTSLSGCLAVVTSYVVLVSLRKHSAGRRQKALSTC 240
Cc      181 VPLVTKACTDPTLYLGLIIVNSGTSLSGCLAVVTSYVVLVSLRKHSAGRRQKALSTC 242
Db      183 VPLVTKACTDPTLYLGLIIVNSGTSLSGCLAVVTSYVVLVSLRKHSAGRRQKALSTC 242
QY      241 SAHFVWVALFPGPCIFITRPTDPSFSDIKVSVFYVTVPPLNPFITYTLRNEEVSAMQ 300
Cc      241 SAHFVWVALFPGPCIFITRPTDPSFSDIKVSVFYVTVPPLNPFITYTLRNEEVSAMQ 302
Db      243 SAHFVWVALFPGPCIFITRPTDPSFSDIKVSVFYVTVPPLNPFITYTLRNEEVSAMQ 302
QY      301 LRQRCV 306
Cc      301 LRQRCV 306
Db      303 LRQRCV 308

```

RESULT 6

AAG72706 standard; Protein; 330 AA.

AAG72706;

31-JUL-2001 (first entry)

Murine OR-like polypeptide query sequence, SEQ ID NO: 2388.

Mouse; olfactory receptor; OR; primary scent determination;
secondary scent determination; polypeptide library; odour receptor;
scent profile; scent fingerprint; scent representation.

Mus musculus.

MO200127158-A2.

19-APR-2001.

06-OCT-2000; 2000WO-US27582.

08-OCT-1999; 99US-0158615.

24-FEB-2000; 2000US-0184809.

(DIGI-) DIGISCENTS.

(YEDA) YEDA RES & DEV CO LTD.

Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

WPI; 2001-290713/30.

New polynucleotides which encode polypeptides involved in olfactory
sensation for identifying olfactory agonists and antagonists -

Example 6; Page 1619-1620; 1857pp; English.

The present sequence is a polypeptide encoded by one of 105 newly mined

CC mouse genes. It was used as a query sequence in a database search of
 CC olfactory receptor (OR)-like sequences. The invention relates to isolated
 CC polynucleotides encoding polypeptides involved in olfactory sensation.
 CC The polynucleotides can be used in screening for olfactory agonists and
 CC antagonists. The methods allow for the determination of primary scents
 CC and the identification of the odour receptors used to detect these
 CC primary scents. The methods also enable determination of secondary scents
 CC and the identification of combinations of odour receptors that are
 CC involved in detecting such secondary scents. This enables the
 CC construction of a scent representation (also called a scent fingerprint
 CC or scent profile), which may be used to re-create and edit scents.
 CC Libraries of olfactory receptors are useful for determining the
 CC interaction pattern of a composition with the receptors, and can be
 CC used for determining differences in the olfactory faculties of different
 CC individuals.
 CC
 SQ Sequence 330 AA;

Query Match 61.6%; Score 992; DB 22; Length 330;
 Best Local Similarity 60.6%; Pred. No. 1.4e-102;
 Matches 183; Conservative 47; Mismatches 72; Indels 0; Gaps 0;

QY 4 LNQRYTEBFVFLGLTDNRVLEMLFMAFSAIYMLTSGNIIIIATVFTPSLHTPMYF 63
 DB 7 INQTSVMSFRLTGLSTNPKVQWAFIFLIFYVLTIVGNIIIVITIIHDRLHTPMYF 66
 QY 64 SNLSFIDICHSYTVPKMLEGLLERKTIISFNCITOLFELHFACARIFLIIYAYDR 123
 DB 67 SNLSFIDICHSYTVPKMLEGLLERKTIISFNCITOLFELHFACARIFLIIYAYDR 126
 QY 124 VAICTPLHYPNVNMNRVCIOLVFALMLGTVHSLGQFELTIRLPYCGPNIIDSYFCDVPL 183
 DB 127 VAICRPLRMTIMNKVCVGLGAMVWTAGTGHISIFSLTILPYCGPNEIDSFCDVPO 186
 QY 184 VIKACTPTVTLGLIIVNMSGTISLSCPLAVTSMVILVLSRKISABGRQALSTGSAH 243
 DB 187 VIELACTPTVTLGLIIVNMSGTISLSCPLAVTSMVILVLSRKISABGRQALSTGSAH 246
 QY 244 FMVVALFPGPCIFITRPTDPSFIDKVVSVFYTAVTPLNPIYTLRNEEVSAMKOLRQ 303
 DB 247 LTVVTLFLGHCFIYSRPSISLPEDKIVSAFPTAITPLNPIYTLRNEEVSAMKOLR 306
 QY 304 RQ 305
 DB 307 RK 308

RESULT 7
 AAG72080 ID AAG72080 standard; Protein; 335 AA.
 XX
 AC AAG72080;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1761.
 XX
 KW Human; olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation.
 XX
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 XX
 PD 19-APR-2001.
 XX
 PP 06-OCT-2000; 2000WO-US27582.
 XX
 PR 08-OCT-1999; 99US-0158615.
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 PI WPI, 2001-290713/30.
 DR

PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 XX
 PS Claim 11; Page 1155-1156; 1857pp; English.

The present sequence is an olfactory receptor which is encoded by
 CC one of a number of novel polynucleotides. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification
 CC of the odour receptors used to detect these primary scents. The methods
 CC also enable determination of secondary scents and the identification of
 CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC faculties of different individuals.

Sequence 335 AA;

Query Match 61.1%; Score 985; DB 22; Length 335;
 Best Local Similarity 63.2%; Pred. No. 8.9e-102;
 Matches 192; Conservative 38; Mismatches 72; Indels 2; Gaps 2;

QY 4 LNQR-VTEFVFLGLTDNRVLEMLFMAFSAIYMLTSGNIIIIATVFTPSLHTPMYF 62
 DB 7 LNQTSVTEFVFLGLTDNRVLEMLFMAFSAIYMLTSGNIIIIATVFTPSLHTPMYF 66
 QY 63 LSNLSFIDICHSYTVPKMLEGLLERKTIISFNCITOLFELHFACARIFLIIYAYDR 122
 DB 67 LSNLSFIDICHSYTVPKMLEGLLERKTIISFNCITOLFELHFACARIFLIIYAYDR 126
 QY 123 VYACTPLHYPNVNMNRVCIOLVFALMLGTVHSLGQFELTIRLPYCGPNIIDSYFCDV 182
 DB 127 VYACRPLRMTIMNKVCVGLGAMVWTAGTGHISIFSLTILPYCGPNEIDSFCDV 186
 QY 183 LVTKLACTPTVTLGLIIVNMSGTISLSCPLAVTSMVILVLSRKISABGRQALSTGSA 241
 DB 187 QVTKLACTPTVTLGLIIVNMSGTISLSCPLAVTSMVILVLSRKISABGRQALSTGSA 246
 QY 242 AHFMVVALFPGPCIFITRPTDPSFIDKVVSVFYTAVTPLNPIYTLRNEEVSAMKOL 301
 DB 247 AHLVVTFLFLGHCFIYSRPSISLPEDKIVSAFPTAITPLNPIYTLRNEEVSAMKOL 306
 QY 302 RQ 305
 DB 307 VGRK 310

RESULT 8
 AAU24670 ID AAU24670 standard; Protein; 311 AA.
 XX
 AC AAU24670;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human olfactory receptor AOLFRI68.
 XX
 KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 KW food additive; cosmetic; fragrance; pharmaceutical additive.
 XX
 OS Homo sapiens.
 XX
 PN WO200168805-A2.
 XX

Query Match	Best Local Similarity	Score	DB	Length	Matches	Local Similarity	Conservative	Mismatches	Indels	Gaps
Query	1	58.2%	Score 938;	DB 22;	Length 311;					
Db	1	55.4%	Pred. No. 1.5e-96;							
Matches	170;	Conservative	59;	Mismatches	76;	Indels	2;	Gaps	1	
Query	1	MDSLNQRTVEFVGLTDNRVLEMLFMAFAIYMLTSGNILLIIATVFTPSLHTPMY	60							
Db	1	MEKIN-NTWETIFMGLSGSPRIEKVCFVPSFFIIILLGNLLMLTCLSNLPSFPMY	58							
Query	61	FELSNLSPFIDICSHSVYVPMLEGLLEKRTISFPDNCITQLPFLMLFACAEIIFLLIYAY	120							
Db	59	FELSLSPFIDICSHSVYVPMLEGLLEKRTISFPDNCITQLPFLMLFACAEIIFLLIYAY	118							
Query	121	DRYVAICTPLHPNPNMNRVCIQVLPALMLGCTVHSLGCTFLITRLPYGPMIIDSIFCD	180							
Db	119	DRYVAICTPLHPNPNMNRVCIQVLPALMLGCTVHSLGCTFLITRLPYGPMIIDSIFCD	178							
Query	141	VPLVILKLACTDLYLNLGILLVTNSGTLSLSCFLAVLTVSWVILVSRKXSAEGRKALSTC	240							
Db	179	VAPVILKLACTDLYLNLGILLVTNSGTLSLSCFLAVLTVSWVILVSRKXSAEGRKALSTC	238							
Query	241	SAHFNVVALFSPGCFIYTRPDTSPSIDKVCVVFYVTVPLNPFYITLRNEEVSAMRQ	300							
Db	239	GSIMAMVVFPPGCFIYTRPDTSPSIDKVCVVFYVTVPLNPFYITLRNEEVSAMRQ	298							
Query	301	LRQROVF 307								
Db	299	LMGRNVF 305								

1D	AA672299	standard; Protein; 311 AA.
1E	AA672291;	
1F	30-JUL-2001	(first entry)
1G	Human olfactory receptor polypeptide, SEQ ID NO: 1972.	
1H	Human; olfactory receptor; OR; primary scent determination;	
1I	secondary scent determination; polypeptide library; odour receptor;	
1J	scent profile; scent fingerprint; scent representation.	
1K	Homo sapiens.	
1L	W0200127158-A2.	
1M	19-APR-2001.	
1N	06-OCT-2000; 2000MO-US27582.	
1O	08-OCT-1999; 99US-0158615.	
1P	24-FEB-2000; 2000US-0184809.	
1Q	(DIGI-) DIGISCENTS.	
1R	(YEDA) YEDA RES & DEV CO LTD.	
1S	Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I,	
1T	WPI, 2001-290713/30.	
1U	New polynucleotides which encode polypeptides involved in olfactory	
1V	sensation for identifying olfactory agonists and antagonists -	
1W	Claim 11; Page 1320-1321; 1857pp; English.	
1X	The present sequence is an olfactory receptor which is encoded by	
1Y	one of a number of novel polynucleotides. The polynucleotides can be	
20	used in screening for olfactory agonists and antagonists. The methods	
21	allow for the determination of primary scents and the identification	
22	of the odour receptors used to detect these primary scents. The methods	
23	also enable determination of secondary scents and the identification of	
24	combinations of odour receptors that are involved in detecting such	
25	secondary scents. This enables the construction of a scent representation	
26	(also called a scent fingerprint or scent profile), which may be used to	
27	re-create and edit scents. Libraries of olfactory receptors are useful	
28	for determining the interaction pattern of a composition with the	
29	receptor, and can be used for determining differences in the olfactory	
30	faculties of different individuals.	
31	Sequence 311 AA;	
32	Query Match 58.2%; Score 938; DB 22; Length 311;	
33	Best Local Similarity 55.4%; Pred. NO. 1.5e-96;	
34	Matches 170; Conservative 59; Mismatches 76; Indels 2; Gaps 1	
35	1 MDSLNQRTVTEVFGLTDNRVLEMLFFMAFSAIMULTLSGNILIIIAIVFTSLHTPMY 60	
36	1 MEKIN--NVTIERIFMGLSGSPRIEKVCVHVSFYIIILGNILMLTVCLSMLFSPMW 58	
37	61 FFLSNLSFIDICHSSVYTPKMLEGILLERKTIISDNCITQLFFHLPAFAEFLIIIVAY 120	
38	59 FFLSFLSPFDICSSSVTAPKMLIVDLADKTIISVGCMLDLGHPFGCEIRIFILVMAV 118	
39	121 DRVVALCPFLHYPNMKNRVCIOALFALMLGATVHSGGTFLTIRLPYCGPNIIDSYPDC 180	
40	119 DRVVALCPFLHYPNMKNRVCIOALFALMLGATVHSGGTFLTIRLPYCGPNIIDSYPDC 178	
41	181 VPLVILACTDPTVLTGLIIVTNSGTTISLCPFLAVTVSYMLVLSLRKHSAGRQALSTC 240	
42	179 VHPVLVALCTERYIIVGVVTVANSGRILAGSVIIIVSYIIVSLRKQSAEGRKALSTC 238	
43	241 SAHEMVVALFEGECFIITRPDTSSIDKIVSVYIYVTVPLANPFITLNEBYSAMKO 300	

receptors (GCREC), while antibodies generated against the polypeptide of the invention are useful for diagnosing a condition or disease associated with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease, CC constipation, AIDS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy. CC AAB71322-AAB71369 represent the GCREC proteins encoded by CC AAF88580-AAF88627 described in the disclosure of the invention.

XX Sequence 311 AA;

Query Match 58.2%; Score 938; DB 23; Length 311;
Best Local Similarity 55.4%; Pred. No. 1.5e-96;
Matches 170; Conservative 59; Mismatches 76; Indels 2; Gaps 1;

1 MSLNQTRETFEVLGLDNRVLEMLFPMASAIYMLTSGNLIITIAVTPPSLHTPMY 60
1 MEKIN--NVTERTFGLSOSPEIEKVCVFVFFIITLIGNLMLTVCLSLFKSPMY 58
61 PFLSNLSFIDICHSVTVPMKLEGLLBERKTIISFNCITOLFPLHFACAEFLIIVAY 120
59 FFLSFLSFVDICVSSVTAPPMIVDLAKKTIISYGCMLQLGVPFGCTEIFILTVAY 118
121 DRYVAICTPLHYPNNWNRVCIQLVPAIMLGTVHSLGQTFITLPIYCGPNITDSYFCD 180
119 DRYVAICKPLHYMTIMNRETCKMMLGTWVGFLHSIIQVALVQLPFCGPNEDHYFCD 178
181 VPLVIACTDPTVYLGIIIVTNSGTISLSCPLAVTSVWVILVSLRKSAEGRKALSTC 240
179 VAPVLAKTLEYIVIGVVATNSGITALSGFVLLISYILVSLKQSAEGRKALSTC 238
241 SAHFVVALFPGPCFIYTRPDTSPSIDKVVSVFTVTPPLNPIYTLRNBEVKSAMQ 300
239 GSHIMAVVIFPGCTFMVRPDTTFSDDKMAVAFYITITPMLNPIIYTLRNBEVKNAMK 298
301 LROROVF 307
299 LMGKNVF 305

RESULT 12

AAU95650 standard; Protein; 311 AA.

XX AAU95650;

DT 02-JUL-2002 (first entry)

DE Human olfactory and pheromone G protein-coupled receptor #137.

XX Human; olfactory and pheromone G protein coupled; receptor;
XX GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
XX anorectic; taste; fragrance; food additive; cosmetic; cell migration;
XX sterility; psychotic disorder; neurological disorder; anxiety;
XX schizophrenia; manic depression; depression; axonal growth;
XX menstrual cycle; appetite sexual motivation; sexual attraction;
XX aggression.

XX Homo sapiens.

PN WO200224726-A2.

PD 28-MAR-2002.

PF 21-SEP-2001; 2001WO-BE00162.

PR 22-SEP-2000; 2000EP-0870211.

XX (CHEM-) CHEMCOM SA.

XX Veithen A;

XX WPI; 2002-330013/36.

DR N-PSDB; ABK68537.

XX Novel pheromone G-protein coupled receptor and receptor-derived
XX agonists, antagonists or inhibitors useful in food or cosmetic products
XX or in the treatment or prevention of neurological disorders such as
XX anxiety and schizophrenia.

PS Disclosure; Page 423-424; 833pp; English.

XX The invention relates to olfactory and pheromone G-protein coupled
XX receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
XX portion and its encoding polynucleotide. Also included are an agonist,
XX antagonist or inhibitor of the GPCR or the polynucleotide, a vector
XX comprising the polynucleotide, a cell transformed by the vector, a non-
XX human mammal comprising a partial or total deletion of the polynucleotide
XX encoding the receptor and screening (detection and possibly, recovering)
XX of compounds which are known or not known to be agonist, antagonists or
XX inhibitors of natural compounds to the GPCR. The receptor-derived
XX agonists, antagonists, inhibitors or compounds are used as an
XX improvement, elimination or substitution of an existing taste and/or a
XX fragrance of (or in) the food and/or cosmetic products. They can also be
XX used in the preparation of medicament in the treatment and/or prevention
XX of a mammalian disorder, such as cell migration, sterility, psychotic and
XX neurological disorders, including anxiety, schizophrenia, manic
XX depression, depression, for promoting axonal growth, nerve cell
XX connection and nerve regeneration for modulating male and female
XX endocrine functions, hormone production and the menstrual cycle, for the
XX prevention or the treatment by stimulation of several mammalian
XX behaviours, such as stimulation or suppression of appetite, sexual
XX motivation, sexual attraction, aggression and for promoting or
XX suppressing chemical communication between organisms. The present
XX sequence is a human olfactory and pheromone GPCR protein sequence.

XX Sequence 311 AA;

Query Match 58.2%; Score 938; DB 23; Length 311;
Best Local Similarity 55.4%; Pred. No. 1.5e-96;
Matches 170; Conservative 59; Mismatches 76; Indels 2; Gaps 1;

1 MSLNQTRETFEVLGLDNRVLEMLFPMASAIYMLTSGNLIITIAVTPPSLHTPMY 60
1 MEKIN--NVTERTFGLSOSPEIEKVCVFVFFIITLIGNLMLTVCLSLFKSPMY 58
61 PFLSNLSFIDICHSVTVPMKLEGLLBERKTIISFNCITOLFPLHFACAEFLIIVAY 120
59 FFLSFLSFVDICVSSVTAPPMIVDLAKKTIISYGCMLQLGVPFGCTEIFILTVAY 118
121 DRYVAICTPLHYPNNWNRVCIQLVPAIMLGTVHSLGQTFITLPIYCGPNITDSYFCD 180
119 DRYVAICKPLHYMTIMNRETCKMMLGTWVGFLHSIIQVALVQLPFCGPNEDHYFCD 178
181 VPLVIACTDPTVYLGIIIVTNSGTISLSCPLAVTSVWVILVSLRKSAEGRKALSTC 240
179 VAPVLAKTLEYIVIGVVATNSGITALSGFVLLISYILVSLKQSAEGRKALSTC 238
241 SAHFVVALFPGPCFIYTRPDTSPSIDKVVSVFTVTPPLNPIYTLRNBEVKSAMQ 300
239 GSHIMAVVIFPGCTFMVRPDTTFSDDKMAVAFYITITPMLNPIIYTLRNBEVKNAMK 298
301 LROROVF 307
299 LMGKNVF 305

RESULT 13

AAU85290 standard; Protein; 311 AA.

XX AAU85290;

DT 08-MAY-2002 (first entry)

DE G-coupled olfactory receptor #151.

XX Human; olfactory G-coupled receptor; sensory perception of odourant;
 KM odour composition; taste composition.
 XX Homo sapiens.
 XX MO200198526-A2.
 XX 27-DEC-2001.
 XX 22-JUN-2001; 2001WO-US20122.
 XX 22-JUN-2000; 2000US-213812P.
 XX 13-MAR-2001; 2001US-0804291.
 XX (SENO-) SENOMTX INC.
 XX Zozulya S, Stryer L;
 XX WPI; 2002-083330/11.
 XX N-P8DB; ABK37649.
 XX
 XX Claim 1; Page 126; 182pp; English.
 XX
 XX The invention relates to a method of representing sensory perception of
 CC one or more odourants. The method comprises: (a) providing a
 CC representative class of n olfactory receptors or ligand binding domains
 CC (LBD) of these receptors; (b) measuring values X1 to Xn representative
 CC of at least one activity of one or more odourants selected from:
 CC (i) binding one or more odourants to the LBD of at least one of the n
 CC olfactory receptors; (ii) activating at least one of the n
 CC olfactory receptors with the one or more odourants; and (iii) blocking at
 CC least one of the n olfactory receptors with the one or more odourants;
 CC and (c) generating a representation of sensory perception from the values
 CC X1 to Xn. The representation of the sensory perception of odourants is
 CC useful for the design and formulation of odour and taste compositions.
 CC AA083140-AA083593 represent human olfactory G-coupled receptor amino acid
 CC sequences of the invention.
 XX
 XX Sequence 311 AA;
 XX
 XX Query Match 58.2%; Score 938; DB 23; Length 311;
 XX Best Local Similarity 55.4%; Pred. No. 1.5e-96;
 XX Matches 170; Conservative 59; Mismatches 76; Indels 2; Gaps 1;
 XX
 XX 1 MDSLNQRTVEFVGLTDNRVLEMLFMAFSAIYMLTSGNLIITIAVTPSPSLATPMY 60
 XX 1 MERKN--NTEFIFMLSGSPREIKVCFVVFSPFIILINLIMLTCLSLTSPSPMY 58
 XX
 XX 61 FPLSLNLFIDICHSVTVPKMLGGLLBRKTSIPNCTIOLPFLHLFACARIFLLIYAY 120
 XX 59 FPLSLFSPFIDICSSVTAPEKMIYDLAKKTSIYVCMQLGQVHFGCTEIFILLVMAV 118
 XX 121 DRYVAICTPLHYPNVNNRVCIOVFAALMGTVHSLGQTEFLIRLPYCGPNIIDSYPD 180
 XX 119 DRYVALCKPLHYMTNNRBTCKNMLGTVVGGFLSHIIQVALVVOQLPFCGPNEIDHYFCD 178
 XX
 XX 181 VPLVIACTDITYLTGIIIVTNSGTSISCLAVVTSYMWIIVSLRKHSABGRKALSTC 240
 XX 179 VAPVIACTACTEYIVGVVVTANSGLTALSFIYLLISYIIIVSLRKQSAEGRKALSTC 238
 XX 241 SAHFVVAALFPGPCITITRPTSPSIDVSVFYTVTPPLNPIYTLRNEEVSAMQ 300
 XX 239 GSHIAVVAVFPGCTFMVNRPTTFSEBDQVAVFYIITPMNPLIYTLRNAEVKNAMK 298
 XX
 XX 301 LROQOVF 307
 XX 299 LMGRAVF 305
 XX
 XX Db

RESULT 14
 ID AAG71471
 AA AAG71471 standard; Protein; 314 AA.
 XX
 XX AAG71471;
 XX
 XX 30-JUL-2001 (first entry)
 XX
 XX Human olfactory receptor polypeptide, SEQ ID NO: 1152.
 XX
 XX Human; olfactory receptor; OR; primary scent determination;
 XX secondary scent determination; polypeptide library; odour receptor;
 XX scent profile; scent fingerprint; scent representation.
 XX
 XX Homo sapiens.
 XX
 XX MO200127158-A2.
 XX 19-APR-2001.
 XX 06-OCT-2000; 2000WO-US27582.
 XX 08-OCT-1999; 99US-0158615.
 XX 24-FEB-2000; 2000US-0184809.
 XX (DIGI-) DIGISCENTS.
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I,
 XX WPI; 2001-290713/30.
 XX
 XX New polynucleotides which encode polypeptides involved in olfactory
 XX sensation for identifying olfactory agonists and antagonists -
 XX
 XX Claim 11; Page 671-672; 1857pp; English.
 XX
 XX The present sequence is an olfactory receptor which is encoded by
 CC one of a number of novel polynucleotides. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification
 CC of the odour receptors used to detect these primary scents. The methods
 CC also enable determination of secondary scents and the identification of
 CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC facilities of different individuals.
 XX
 XX Sequence 314 AA;
 XX
 XX Query Match 57.7%; Score 929; DB 22; Length 314;
 XX Best Local Similarity 53.1%; Pred. No. 1.6e-95;
 XX Matches 165; Conservative 67; Mismatches 79; Indels 0; Gaps 0;
 XX
 XX 1 MDSLNQRTVEFVGLTDNRVLEMLFMAFSAIYMLTSGNLIITIAVTPSPSLATPMY 60
 XX 1 MDVGNKSTMSSEFVLLGLNSMELQWFFMVVFSLLVVAATVNGSLIVITVYDPHLSPMY 60
 XX
 XX 61 FPLSLNLFIDICHSVTVPKMLGGLLBRKTSIPNCTIOLPFLHLFACARIFLLIYAY 120
 XX 61 FPLTNLSIIDMSLAFAPKMTITDYLGHKTSIFPGCTIOLPFLHLFGTEIILMAMSF 120
 XX 121 DRYVAICTPLHYPNVNNRVCIOVFAALMGTVHSLGQTEFLIRLPYCGPNIIDSYPD 180
 XX 121 DRYVAICTPLHYASISPOVCALVAVSMINGVHMSQVIFALTLPCGPPEVDSFCD 180
 XX
 XX 181 VPLVIACTDITYLTGIIIVTNSGTSISCLAVVTSYMWIIVSLRKHSABGRKALSTC 240
 XX 181 LPVVFQIACVDIVYVGLFMISTSGIILSCFIVLNSYVIVLVYVKKHSSRGSSKALSTC 240
 XX
 XX Db

[illegible]

RESULT 15

ID	ABP95834	standard; Protein; 314 AA.
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96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

AC ABP95834;

DT 06-MAR-2003 (first entry)

Human GPCR polypeptide SEQ ID NO 478.

KM Human; GPCR; G protein coupled receptor; signal transduction; olfactory
 KM drug development; gustatory; taste; fragrance; receptor.

OS Homo sapiens

PN W0200216548-A2.

PD 28-FEB-2002.

30-JUL-2001; 2001WO-IB01446.

PR 04-AUG-2000; 2000JP-0237818.

XX
XX (MTC) / TAPAN CAT & PENCUNTO

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

Haga T, Takeda S, Mitaku S;

DR WPI; 2002-304118/34.

DR N-PSDB; ABZ43108

PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development -

PS Claim 10; SEQ ID NO 478; 97pp + Sequence Listing; Japanese.

CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins
CC (ABP95596-ABP95942) by extracting open-reading frames containing 6-8
CC transmembrane domains with 250-1000 amino acid residues to give a gene
CC homologous with a known GPCR gene. The receptor proteins and encoded
CC genes are useful for studying in vivo signal transduction mechanism and
CC identifying targets for drug development e.g. based on olfactory and
CC gustatory receptors in form of agonists and antagonists by screening
CC intrinsic and extrinsic ligands as bitter taste inhibitors, taste
CC enhancers and fragrance improvers.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.

SQ Sequence 314 AA;

Query Match	57.7%	Score 929	DB 23	Length 314
Best Local Similarity	53.1%	Pred. No. 1.6e-95		
Matches .165	Conservative 67	Mismatches 79	Indels 0	Gaps 0

[illegible]

```

Db      6.  FLTNLSIIDMSLASPATKMTDYLTHKHTISFGDGLTQIFLHLPTGTEIILMMAMSE 120
Qy      121  DRVVAICTPLHPNWNMMKVCQLVFMALMGTVHSLGQTLTLRLPYCCPNIIIDSYFCD 180
Db      121  DRIAIACPLHVASVISPQVCALVWAMINGVHMSQVIFALTLPFCGEVDSFFCD 180
Qy      181  VPIVIKLACTDYLTGILIVNMSGTISLSCFLAVTSMVILVSLRKHSAGROKALSTC 240
Db      181  LPVVFQACADYTVLGLFMISTSGIATLSCLPIVLENSVIVLVLVVKHSSRGSSKALSTC 240
Qy      241  SAHFHVVVALFPGBCIFITYRPDTSIDKVVSVPTVTVPLNPFITTLNBEYKSAAMKQ 3000
Db      241  TAFHFIVVLPFGBCIFITYMPLSSFLTKIISVFPITPTLPNPIYTLRNQEVKIAMRK 3000
Qy      301  LROROVFPTRKS 311
Db      301  LKRRFLNENKA 311

```

Search completed: August 12, 2003, 16:06:45
Job time : 85 secs

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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:01:06 ; Search time 98 seconds

(without alignments)
824.188 Million cell updates/sec

Title: US-09-807-132-4

Perfect score: 1611

Sequence: 1 MDSLNQRTVTEVFGLTDN.....VKSAMKQLRQGVFTKSTY 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1611	100.0	313	4	Q8NGC2
2	1380	85.7	308	11	Q9R0K3
3	1112	69.0	213	4	Q96R62
4	1016	63.1	310	11	Q9R0K4
5	992	61.6	313	11	Q9R0K5
6	938	58.2	311	4	Q8NH73
7	931	57.8	318	11	Q8VF96
8	929	57.7	314	4	Q8NGD2
9	927.5	57.6	310	4	Q8NGD5
10	921	57.2	308	11	Q8VGN8
11	920	57.1	326	11	Q8VF11
12	919	57.0	324	4	Q8NH41
13	918	56.7	309	11	Q8VEZ3
14	914	56.6	321	11	Q8VEX0
15	912	56.6	324	11	Q8VEX3
16	911	56.5	309	11	Q8VEZ2

17	909	56.4	309	11	Q8VGN7	Q8VGN7 mus musculus
18	906	56.2	318	4	Q8NG74	Q8NG74 homo sapien
19	904	56.1	309	11	Q8VEY5	Q8VEY5 mus musculus
20	902	56.0	304	11	Q8VGP3	Q8VGP3 mus musculus
21	900	55.9	318	4	Q8NGNO	Q8NGNO homo sapien
22	897.5	55.7	321	11	Q8VEX1	Q8VEX1 mus musculus
23	897	55.7	309	11	Q8K500	Q8K500 mus musculus
24	894.5	55.5	307	11	Q8VGN3	Q8VGN3 mus musculus
25	893	55.4	302	11	Q9R0K1	Q9R0K1 mus musculus
26	893	55.4	311	4	Q8NGD4	Q8NGD4 homo sapien
27	891	55.3	305	11	Q8VGP2	Q8VGP2 mus musculus
28	889.5	55.2	318	11	Q8VFC7	Q8VFC7 mus musculus
29	889	55.2	308	4	Q8VEX1	Q8VEX1 homo sapien
30	888.5	55.2	303	11	Q8VFP9	Q8VFP9 mus musculus
31	888	55.1	311	4	Q8NGD6	Q8NGD6 homo sapien
32	883	54.8	303	11	Q8VFP8	Q8VFP8 mus musculus
33	883	54.8	307	11	Q8VGP4	Q8VGP4 mus musculus
34	882	54.7	323	11	Q8VET4	Q8VET4 mus musculus
35	880.5	54.7	313	4	Q8NH05	Q8NH05 homo sapien
36	878	54.5	315	4	Q8NGC6	Q8NGC6 homo sapien
37	877	54.4	308	11	Q8VFT3	Q8VFT3 mus musculus
38	877	54.4	311	11	Q8VFP9	Q8VFP9 mus musculus
39	877	54.4	311	11	Q8VFN1	Q8VFN1 mus musculus
40	874	54.3	303	11	Q8VFP4	Q8VFP4 mus musculus
41	873	54.2	310	11	Q8VFP7	Q8VFP7 mus musculus
42	873	54.2	314	4	Q8NGE8	Q8NGE8 homo sapien
43	872	54.1	311	11	Q8VGT4	Q8VGT4 mus musculus
44	871	54.1	324	11	Q9R0G2	Q9R0G2 marmota mar
45	869	53.9	308	11	Q9R0K2	Q9R0K2 mus musculus

ALIGNMENTS

RESULT 1
Q8NGC2 PRELIMINARY; PRT; 313 AA.

AC Q8NGC2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsubumai S., Aburatani H., Asai K., Akiyama Y.;
RT Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB065895; BAC06111.1;
DR InterPro; IPR000276; GPCR Rhodops.
DR InterPro; IPR000985; Lectin_lega.
DR Pfam; PR00001; 7cm_1; 1.
DR PRINTS; PR00237; GPCRHOPOBN.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPE_F1_2; 1.
DR PROSITE; PS00308; LECTIN_LEGUM_ALPHA; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 313 AA; 35466 MW; 59A922BBA6978452 CRC64;

Query Match 100.0%; Score 1611; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 3.2e-137;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSLNQRTVTEVFGLTDNRLVLEMLFPMAFSAIYMLTSGNIIIIITATVTPSPATPMY 60
DB 1 MDSLNQRTVTEVFGLTDNRLVLEMLFPMAFSAIYMLTSGNIIIIITATVTPSPATPMY 60
QY 61 FPLSNLSFDIDICHSSVTVPKMLEGLLLEKRTISFDNCITTOLEFHLFAACAFILLIIVAY 120

Db	61	FFLSNLSFIDICHSSTVTPKMLEGLLEKRTISPNCITQLFPHLFACAEIPLLIVAY	120
Qy	121	DRVVALCTPLHYNNMMNMCVCTQLVPAALGGTSHSLGQTELTITRLPVCGNIIIDSYFCD	180
Db	121	DRVVALCTPLHYNNMMNMCVCTQLVPAALGGTSHSLGQTELTITRLPVCGNIIIDSYFCD	180
Qy	181	VPLVILKLACTDYLVTGILIVTNSGTTSLSCFLAVVTSYMWIIIVSLRKHSABGRKALSTC	240
Db	181	VPLVILKLACTDYLVTGILIVTNSGTTSLSCFLAVVTSYMWIIIVSLRKHSABGRKALSTC	240
Qy	241	SAHFMMVVALEFGCECIEFYTRPDTSFSIDKVSVFVTVTPLNPLPIYTLRNEEVSAMKQ	300
Db	241	SAHFMMVVALEFGCECIEFYTRPDTSFSIDKVSVFVTVTPLNPLPIYTLRNEEVSAMKQ	300
Qy	301	LROROVFFTKSYT 313	
Db	301	LROROVFFTKSYT 313	

RESULT 2	09R0K3	PRELIMINARY;	PRT;	308 AA.
ID	09R0K3			
AC	09R0K3;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Odorant receptor MOR83 (Olfactory receptor MOR244-3).			
GN	MOR83.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCHI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129-SVJ;			
RA	Tsuboi A., Yoshihara S., Yamazaki N., Kasai H., Asai-Tsuboi H.,			
RA	Komatsu M., Seizawa S., Ishii T., Matsuda Y., Nagawa F., Sakano H.;			
RT	"Olfactory neurons expressing closely linked and homologous odorant			
RT	receptor genes tend to project their axons to neighboring glomeruli on			
RT	the olfactory bulb."			
RL	J. Neurosci. 0:0-0(1999).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RA	Zhang X., Firestein S.J.;			
RT	"The olfactory receptor gene superfamily of the mouse."			
RL	Nat. Neurosci. 0:0-0(2002).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Adams M.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB030894; BA86125.1; -;			
DR	EMBL; AY073295; AAL60958.1; -;			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHDOPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.			
DR	Receptor.			
SO	SEQUENCE 308 AA; 35015 MW; 73CPBD1630540C5 CRC64;			
Query Match	85.7%;	Score 1380;	DB 11;	Length 308;
Best Local Similarity	85.6%;	Pred. No. 2.1e-116;		
Matches 262;	Conservative 20;	Mismatches 24;	Indels 0;	Gaps 0;
QY	1	MSLSINQRYVEFVFLGTDNRVYLEMFPAFSAIYMLTLTSGNIIILIAITVFTPSLHTPMY	60	
DB	1	MGALNQRYVEFVFLGTDNRVYLEMFPAFSAIYMLTLTSGNIIILIAITVFTPSLHTPMY	60	
QY	61	FFLSINLSFDIDCHSSVTVPRMELGLLEKRTISPNQCITQLEFLHFACAISFLIIVAY	120	
DB	61	FFLSINLSFDIDCHSSVTVPRMELGLLEKRTISPNQCITQLEFLHFACAISFLIIVAY	120	

[illegible]

ID	Q96R62	PRELIMINARY;	PRT;	213 AA.
AC	Q96R62;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Olfactory receptor (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,			
RA	Shmulevich D., Alkon R., Steinfath M., O'Brien J.K., Radloff U.,			
RA	Lehrach H., Olander Z., Glusman G., Lancelot D., Shamir R.;			
RT	DBF02: A Practical Scheme for Deciphering Families of Genes.;			
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBD databases.			
DR	EMBL; AF399581; AAK95066.1; -			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.			
KM	Receptor.			
FT	NON_TER	1	1	
FT	NON_TER	213	213	
SQ	SEQUENCE	213 AA;	23792 MW;	74819DPA82D5230DB CRC64;
Query Match		69.0%;	Score 1112;	DB 4; Length 213;
Best Local Similarity		100.0%;	Prod. No. 2e-92;	
Matches	213; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	68 FIDICHSVVTPKMLEGLLEKRTISFDNCITQQLFHLFACAEIFLLIIIVAYDRYVAIC			127
DB	1 FIDICHSVVTPKMLEGLLEKRTISFDNCITQQLFHLFACAEIFLLIIIVAYDRYVAIC			60
QY	128 TELHYPNVMNRVCIQLVFAIMLGTVHSLGOTFLTTLTPVCGPIIIDSYPEDVPLVTKL			187
DB	61 TELHYPNVMNRVCIQLVFAIMLGTVHSLGOTFLTTLTPVCGPIIIDSYPEDVPLVTKL			120
QY	188 ACTDTYVLGLIIVTNSGTTSLSCFLAVTVTSMVILVLSLRKHSABEGROKALSTCSAHFMVY			247
DB	121 ACTDTYVLGLIIVTNSGTTSLSCFLAVTVTSMVILVLSLRKHSABEGROKALSTCSAHFMVY			180
QY	248 ALFPGPCIFITYRPDTSFSDIKVSVFPTVTVTP			280
DB	181 ALFPGPCIFITYRPDTSFSDIKVSVFPTVTVTP			213
RESULT 4				
ID	Q9ROK4	PRELIMINARY;	PRT;	310 AA.
AC	Q9ROK4;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			

DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE Odorant receptor MOR10 (Olfactory receptor MOR244-2).
 GN MOR10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Tsuboi A., Yoshihara S., Yamazaki N., Kasai H., Asai-Tsuboi H.,
 RA Komatsu M., Serizawa S., Ishii T., Matsuda Y., Nagawa F., Sakano H.,
 RT "Olfactory neurons expressing closely linked and homologous odorant
 RT receptor genes tend to project their axons to neighboring glomeruli on
 RT the olfactory bulb."
 RL J. Neurosci. 0:0-0(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.,
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Adams M.,
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030893; BAA86124.1; -.
 DR EMBL; AY073294; AAL60957.1; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 DR KX Receptor.
 SQ SEQUENCE 310 AA; 34979 MW; BAD597BB82AFB39 C3C64;
 Query Match 63.1%; Score 1016; DB 11; Length 310;
 Best Local Similarity 62.6%; Pred. No. 1.3e-83;
 Matches 189; Conservative 45; Mismatches 68; Indels 0; Gaps 0;
 QY 4 INQTRTEVFVGLTNDRLVLEMLFMAFSAIYMLTSGNIIITIAVTPSPSLHTPMYFPL 63
 DB 7 INQTSVMSFRLTGLSTNPLVQMAVFIFLIFVLTIVGNILVITTIYDRRLHTPMYFPL 66
 QY 64 SNLSFIDICHSSTVTPKMLEGLLEKRTISPDNCITQLEFHLFACABIFLLIIVADRY 123
 DB 67 SNLSFIDVCHSTVTPKMLSDTFSEKLIISFDACVQGFHLFACTEIFLLTWAYDXY 126
 QY 124 VAICPLRYHPNMMNRVCIOVFAIMLGSTVSLGOTPLTIRLPGCGPIIDSYCDVPL 183
 DB 127 VAICPLRYMTIMNMKVCIMLAALMTGTGTHSISLTSLTKLPYCGPDELDSFCDVQ 186
 QY 184 VIKLACTDYTLGILIVTNSGTISLSCFLAVTSMVILVSLRKHSABGRKALSTCSAH 243
 DB 187 VIKLACTDRIITELIVNSGILSVCFVLLVSTAVILVSLRQGISDGRKALSTCSAH 246
 QY 244 FNVVALFPGPCIFITRPTSPSIDKVSVFYTVTPPLNFIYTLRNEEVSAMKOLRQ 303
 DB 247 LTVVTLFLGHCIFIVSRPSTSLPEDKIVSAFPTATPLNFIYTLRNEEVSAMKOLR 306
 QY 304 RQ 305
 DB 307 RR 308

RESULT 5

Q9R0K5 PRELIMINARY; PRT; 313 AA.
 AC Q9R0K5;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE Odorant receptor MOR28 (Olfactory receptor MOR244-1).
 GN MOR28.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Tsuboi A., Yoshihara S., Yamazaki N., Kasai H., Asai-Tsuboi H.,
 RA Komatsu M., Serizawa S., Ishii T., Matsuda Y., Nagawa F., Sakano H.,
 RT "Olfactory neurons expressing closely linked and homologous odorant
 RT receptor genes tend to project their axons to neighboring glomeruli on
 RT the olfactory bulb."
 RL J. Neurosci. 0:0-0(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.,
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Adams M.,
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030892; BAA86123.1; -.
 DR EMBL; AY073251; AAL60914.1; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 DR KX Receptor.
 SQ SEQUENCE 313 AA; 35397 MW; F5AA7286F3A40ABE CRC64;
 Query Match 61.6%; Score 992; DB 11; Length 313;
 Best Local Similarity 60.6%; Pred. No. 1.9e-81;
 Matches 183; Conservative 47; Mismatches 72; Indels 0; Gaps 0;
 QY 4 INQTRTEVFVGLTNDRLVLEMLFMAFSAIYMLTSGNIIITIAVTPSPSLHTPMYFPL 63
 DB 7 INQTSVMSFRLTGLSTNPLVQMAVFIFLIFVLTIVGNILVITTIYDRRLHTPMYFPL 66
 QY 64 SNLSFIDICHSSTVTPKMLEGLLEKRTISPDNCITQLEFHLFACABIFLLIIVADRY 123
 DB 67 SNLSFIDVCHSTVTPKMLSDTFSEKLIISFDACVQGFHLFACTEIFLLTWAYDXY 126
 QY 124 VAICPLRYHPNMMNRVCIOVFAIMLGSTVSLGOTPLTIRLPGCGPIIDSYCDVPL 183
 DB 127 VAICPLRYMTIMNMKVCIMLAALMTGTGTHSISLTSLTKLPYCGPDELDSFCDVQ 186
 QY 184 VIKLACTDYTLGILIVTNSGTISLSCFLAVTSMVILVSLRKHSABGRKALSTCSAH 243
 DB 187 VIKLACTDRIITELIVNSGILSVCFVLLVSTAVILVSLRQGISDGRKALSTCSAH 246
 QY 244 FNVVALFPGPCIFITRPTSPSIDKVSVFYTVTPPLNFIYTLRNEEVSAMKOLRQ 303
 DB 247 LTVVTLFLGHCIFIVSRPSTSLPEDKIVSAFPTATPLNFIYTLRNEEVSAMKOLR 306
 QY 304 RQ 305
 DB 307 RR 308

RESULT 6

Q8NH73 PRELIMINARY; PRT; 311 AA.
 AC Q8NH73;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE Seven transmembrane helix receptor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arica M., Putani K., Matsumoto S.,
RA Tautsumi S., Aburatani H., Asai K., Akiyama Y.,
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB065516; BAC05764.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 311 AA; 35138 MW; 8EAA48B9C3B081BC CRC64;

Query Match 58.2%; Score 938; DB 4; Length 311;
Best Local Similarity 55.4%; Pred. No. 1,4e-76;
Matches 170; Conservative 59; Mismatches 76; Indels 2; Gaps 1;

QY 1 MDSLNGRTVTEFVFLGTDNRVLEMLFPMAPSAIYMLTSGNLIITIAVTFPSLHTPMY 60
DB 1 MEKIN--NTERFIFGLSGNPEVEKVCVFVFFFIILGLNLIIMLTVCGLNLFKSPMY 58
QY 61 FFLSNLSFIDICHSYTVPMKLEGLLBERKTSFNDCTQLFFLHLPACAEIFLLIIVAY 120
DB 59 FFLSFLSFVDICYSSTVAPKMIIDLVKKKTSYVGCMLQLGVHFGCTEIFILTVMAY 118
QY 121 DRYVAICTPLHYPNVNMKVCIOLVFALMLGSTVHSLGQTFILRLPYCGPNIIDSYFCD 180
DB 119 DRYVAICTPLHYPNVNMKVCIOLVFALMLGSTVHSLGQTFILRLPYCGPNIIDSYFCD 178
QY 181 VPLVIACTPLHYPNVNMKVCIOLVFALMLGSTVHSLGQTFILRLPYCGPNIIDSYFCD 240
DB 179 VHPVLKACTDITYIGVIFVANSGLTALGSPVILLISYVILMSLRKQSEGRKALSTC 238
QY 241 SAHFNVVALFPGPCIFLYTRPDTSPSIDKVSVFYTVVPLNPFYTLNREBVSAMQ 300
DB 239 GSHIAVAVIIFPGPCIFLYTRPDTSPSIDKVSVFYTVVPLNPFYTLNREBVSAMQ 298
QY 301 LRORQ 307
DB 299 LMGKNVF 305

RESULT 7
Q8VF96 PRELIMINARY; PRT; 318 AA.
ID Q8VF96
AC Q8VF96
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Olfactory receptor MOR26-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073638; AAL61301.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.

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SQ SEQUENCE 318 AA; 36298 MW; 621BDE95D4CAA826 CRC64;

Query Match 57.8%; Score 931; DB 11; Length 318;
Best Local Similarity 55.7%; Pred. No. 6.1e-76;
Matches 170; Conservative 58; Mismatches 75; Indels 2; Gaps 1;

QY 1 MDSLNGRTVTEFVFLGTDNRVLEMLFPMAPSAIYMLTSGNLIITIAVTFPSLHTPMY 60
DB 8 MEENV--NTERFIFGLSGNPEVEKVCVFVFFFIILGLNLIIMLTVCGLNLFKSPMY 65
QY 61 FFLSNLSFIDICHSYTVPMKLEGLLBERKTSFNDCTQLFFLHLPACAEIFLLIIVAY 120
DB 66 FFLNLSFVDICYSSTVAPKMIIDLVKKKTSYVGCMLQLGVHFGCTEIFILTVMAY 125
QY 121 DRYVAICTPLHYPNVNMKVCIOLVFALMLGSTVHSLGQTFILRLPYCGPNIIDSYFCD 180
DB 126 DRYVAICTPLHYPNVNMKVCIOLVFALMLGSTVHSLGQTFILRLPYCGPNIIDSYFCD 185
QY 181 VPLVIACTDITYIGVILVNSGTLISLCPAVNTSYVILVSLRKHSAGRQALSTC 240
DB 186 VHPVLKACTDITYIGVIFVANSGLTALGSPVILLISYVILMSLRKQSEGRKALSTC 245
QY 241 SAHFNVVALFPGPCIFLYTRPDTSPSIDKVSVFYTVVPLNPFYTLNREBVSAMQ 300
DB 246 GSHIAVAVIIFPGPCIFLYTRPDTSPSIDKVSVFYTVVPLNPFYTLNREBVSAMQ 305
QY 301 LRORQ 305
DB 306 LMARK 310

RESULT 8
Q8NGD2 PRELIMINARY; PRT; 314 AA.
ID Q8NGD2
AC Q8NGD2
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arica M., Putani K., Matsumoto S.,
RA Tautsumi S., Aburatani H., Asai K., Akiyama Y.,
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB065883; BAC06101.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 314 AA; 35357 MW; 946877CDB260EC59 CRC64;

Query Match 57.7%; Score 929; DB 4; Length 314;
Best Local Similarity 53.1%; Pred. No. 9.1e-76;
Matches 165; Conservative 67; Mismatches 79; Indels 0; Gaps 0;

QY 1 MDSLNGRTVTEFVFLGTDNRVLEMLFPMAPSAIYMLTSGNLIITIAVTFPSLHTPMY 60
DB 1 MOVGNSTSEFVLGLSSNWELOMFVFLVAVATVNSGLVITVIVDPHLSHPY 60
QY 61 FFLSNLSFIDICHSYTVPMKLEGLLBERKTSFNDCTQLFFLHLPACAEIFLLIIVAY 120
DB 61 FFLTNLSITDMSLASATPKMITDVLTGKITSFPGCLTQIFFLHLPCTETIILMAMSF 120
QY 121 DRYVAICTPLHYPNVNMKVCIOLVFALMLGSTVHSLGQTFILRLPYCGPNIIDSYFCD 180

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Db 121 DRYIAICKELEHVASISPCVCAVAVASWIMVGHSMQYIFALTLPFCGPYEVDSFCD 180
 QY 181 VPLVITACTDPTVLTGILVNTSGTISLSCFLAVTSMYILVSLKSGAEGROKALSTC 240
 Db 181 LPLVFCACADYVVLGLFMISTGIIALSCFIYLFENSXYIVLVTVGHSSRSSKALSTC 240
 QY 241 SAHFVVALFPGCFIYTRPDTSPSIDKVSVFYVTVPLNPFYITLRNEBVKSAAMQ 300
 Db 241 TAFHIVVLPFGGCFIYVMPPLSSFLTDKILSVFIYITFTLNPITTLRNDGEVKIANK 300
 QY 301 LKROVFPFYS 311
 Db 301 LKRRPLNFYKA 311

RESULT 9

Q8NGD5 PRELIMINARY; PRT; 310 AA.
 AC Q8NGD5; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Seven transmembrane helix receptor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsubsumi S., Aburatani H., Asai K., Akiyama Y.,
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB065880; BAC06098.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G PROTEIN_RECP_F1_2; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 310 AA; 35052 MW; AA7B06959BFE8E0D CRC64;

Query Match 57.6%; Score 927.5; DB 4; Length 310;
 Best Local Similarity 55.0%; Pred. No. 1.2e-75;
 Matches 170; Conservative 60; Mismatches 78; Indels 1; Gaps 1;

QY 1 MSLAQRTAEVFLGLTNRVLEMLFFMAFSAIYMLTSGNIIITATVTPSLH-TTPM 59
 Db 1 MDPQYSLVSEFVLHGLCTSRHLONFELFFFGVVAIMGLNLLIVTVISDPCLHSSPM 60
 QY 60 YFFLNLSPFIDICHSVTVPKMLEGLLEKRTISPNCTQLFPLLPACAEFILIIYA 119
 Db 61 YFLNLGLFLDMLWLASFAFPKMRDPLSLQKILISFGCCMAQIFLHFTGGAEMVLLVSWA 120
 QY 120 YDRVAICTPLHYPNVMNRKVCIOVFALMLGTVHSLGQTLTIRLPYCGENIIDSYFC 179
 Db 121 YDRVAIICKPLHYMLTMSQTCIRLVASGVVGFHVSQVAFYNLPGCNENVDSPFC 180
 QY 180 DPLVITKACTDPTVLTGILVNTSGTISLSCFLAVTSMYILVSLKSGAEGROKALST 239
 Db 181 DPLVITKACTDPTVLTGILVNTSGTISLSCFLAVTSMYILVSLKSGAEGROKALST 240
 QY 240 CSAHFVVALFPGCFIYTRPDTSPSIDKVSVFYVTVPLNPFYITLRNEBVKSAAMK 299
 Db 241 CSAHFVVALFPGCFIYTRPDTSPSIDKVSVFYVTVPLNPFYITLRNEBVKSAAMK 300
 QY 300 QLRQVFPF 308
 Db 301 KLQNRRTVF 309

RESULT 10

Q8VGN8 PRELIMINARY; PRT; 308 AA.
 AC Q8VGN8; 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Olfactory receptor MOR227-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.,
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073108; AAL6077.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 308 AA; 34374 MW; BE466A13B5D05116 CRC64;

Query Match 57.2%; Score 921; DB 11; Length 308;
 Best Local Similarity 55.2%; Pred. No. 4.7e-75;
 Matches 164; Conservative 60; Mismatches 73; Indels 0; Gaps 0;

QY 5 NOTRTVEVFLGLTNRVLEMLFFMAFSAIYMLTSGNIIITATVTPSLHTTPYFELS 64
 Db 3 KKNNTTBLIFGLFQDPPEVQKCFPLFLPVYIATLGLNSLIVAVSISKTLHSPMYFELS 62
 QY 65 NLSFIDICHSVTVPKMLEGLLEKRTISPNCTQLFPLLPACAEFILIIYAVDRYV 124
 Db 63 SLISVEICYSSTIYKFTDILVKKVKTISLGGCLAQIFSHFLGVAETLLVMAVDYRV 122
 QY 125 AICPLAHYPNVMNRKVCIOVFALMLGTVHSLGQTLTIRLPYCGENIIDSYPGCVPLV 184
 Db 123 AICKPLAHYMNISRQCHMLVGGSLGGLHSHIIITITPLPGGPRVIDHYFCDLPL 182
 QY 185 IKLACTDPTVLTGILVNTSGTISLSCFLAVTSMYILVSLKSGAEGROKALSTCSAHF 244
 Db 183 FKLACTDPTFMGVVMAVNSGLISISLPLVSSVAIILISRKHSABGRRLALSTCSAHF 242
 QY 245 MVVALFPGCFIYTRPDTSPSIDKVSVFYVTVPLNPFYITLRNEBVKSAAMKQ 301
 Db 243 TVVILFFQPAFLVLRPSSFTBDKLVAVFTVITPLNPFYITLRNEBVKSAAMKQ 299

RESULT 11

Q8VF11 PRELIMINARY; PRT; 326 AA.
 AC Q8VF11; 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Olfactory receptor MOR246-5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.,
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.

RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073730; AAL61393.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR000985; Lectin_lega.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 DR PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
 KM Receptor

SO

SEQUENCE 326 AA; 37023 MW; DE2E1F4B7B4EFC5 CRC64;

Query Match

Best Local Similarity 57.4%; Score 920; DB 11; Length 326;
 Matches 165; Conservative 61; Mismatches 81; Indels 0; Gaps 0;

QY 1 MSLSNTRVTEFVFLGTDNRVLEMLFPMASAIYMLTSGNIIITATVFTPSLHTPMY 60
 DB 1 MERLNHSRVTEFVFLGTDNRVLEMLFPMASAIYMLTSGNIIITATVFTPSLHTPMY 60
 QY 61 FPLSNLSFIDCHSVTVPKMLBGLLERTISFNDCTQLFPLHACAEIFLLIIVAY 120
 DB 61 FPLSNLSFIDCHSVTVPKMLBGLLERTISFNDCTQLFPLHACAEIFLLIIVAY 120
 QY 121 DRYVAICTPLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCD 180
 DB 121 DRYVAICTPLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCD 180
 QY 121 DRYVAICTPLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCD 180
 DB 121 DRYVAICTPLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCD 180
 QY 181 VPLVTLACIDTYLTLGILVTSNGTISLSCFLAVTSYVIVLSLRKHSABGROKALSTC 240
 DB 181 VPLVTLACIDTYLTLGILVTSNGTISLSCFLAVTSYVIVLSLRKHSABGROKALSTC 240
 QY 181 LPLVTLACIDTYLTLGILVTSNGTISLSCFLAVTSYVIVLSLRKHSABGROKALSTC 240
 DB 181 LPLVTLACIDTYLTLGILVTSNGTISLSCFLAVTSYVIVLSLRKHSABGROKALSTC 240
 QY 241 SAHFVVALFPGCFIYTRPDTSPSIDKVSVEYTVVTPPLNPFYTLRNEEYKAMQ 300
 DB 241 TSHTVTLVLFPGCFIYTRPDTSPSIDKVSVEYTVVTPPLNPFYTLRNEEYKAMQ 300
 QY 301 LRQROVF 307
 DB 301 LRQROVF 307
 QY 301 KISNOVF 307
 DB 301 KISNOVF 307

RESULT 12

Q8NH41 ID C8NH41 PRELIMINARY; PRT; 324 AA.

AC C8NH41;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Seven transmembrane helix receptor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

SEQUENCE FROM N.A.

RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tautami S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB065560; BAC05798.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR000985; Lectin_lega.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 DR PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
 KM Receptor; Transmembrane.

SO SEQUENCE 324 AA; 36483 MW; 76ACFCF465AA07A9F CRC64;

Query Match

Best Local Similarity 57.0%; Score 919; DB 4; Length 324;

Best Local Similarity 56.2%; Pred. No. 7.4e-75;
 Matches 171; Conservative 50; Mismatches 83; Indels 0; Gaps 0;

QY 1 MSLSNTRVTEFVFLGTDNRVLEMLFPMASAIYMLTSGNIIITATVFTPSLHTPMY 60
 DB 1 MERLNHSRVTEFVFLGTDNRVLEMLFPMASAIYMLTSGNIIITATVFTPSLHTPMY 60
 QY 61 FPLSNLSFIDCHSVTVPKMLBGLLERTISFNDCTQLFPLHACAEIFLLIIVAY 120
 DB 61 FPLSNLSFIDCHSVTVPKMLBGLLERTISFNDCTQLFPLHACAEIFLLIIVAY 120
 QY 121 DRYVAICTPLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCD 180
 DB 121 DRYVAICTPLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCD 180
 QY 121 DRYVAICTPLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCD 180
 DB 121 DRYVAICTPLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCD 180
 QY 181 VPLVTLACIDTYLTLGILVTSNGTISLSCFLAVTSYVIVLSLRKHSABGROKALSTC 240
 DB 181 VPLVTLACIDTYLTLGILVTSNGTISLSCFLAVTSYVIVLSLRKHSABGROKALSTC 240
 QY 181 LPLVTLACIDTYLTLGILVTSNGTISLSCFLAVTSYVIVLSLRKHSABGROKALSTC 240
 DB 181 LPLVTLACIDTYLTLGILVTSNGTISLSCFLAVTSYVIVLSLRKHSABGROKALSTC 240
 QY 241 SAHFVVALFPGCFIYTRPDTSPSIDKVSVEYTVVTPPLNPFYTLRNEEYKAMQ 300
 DB 241 TSHTVTLVLFPGCFIYTRPDTSPSIDKVSVEYTVVTPPLNPFYTLRNEEYKAMQ 300
 QY 301 LRQROVF 304
 DB 301 LRQROVF 304
 QY 301 KISNOVF 304
 DB 301 KISNOVF 304

RESULT 13

Q8VEZ3 ID C8VEZ3 PRELIMINARY; PRT; 309 AA.

AC C8VEZ3;
 DT 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Olfactory receptor MOR228-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;
 RA "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]

SEQUENCE FROM N.A.

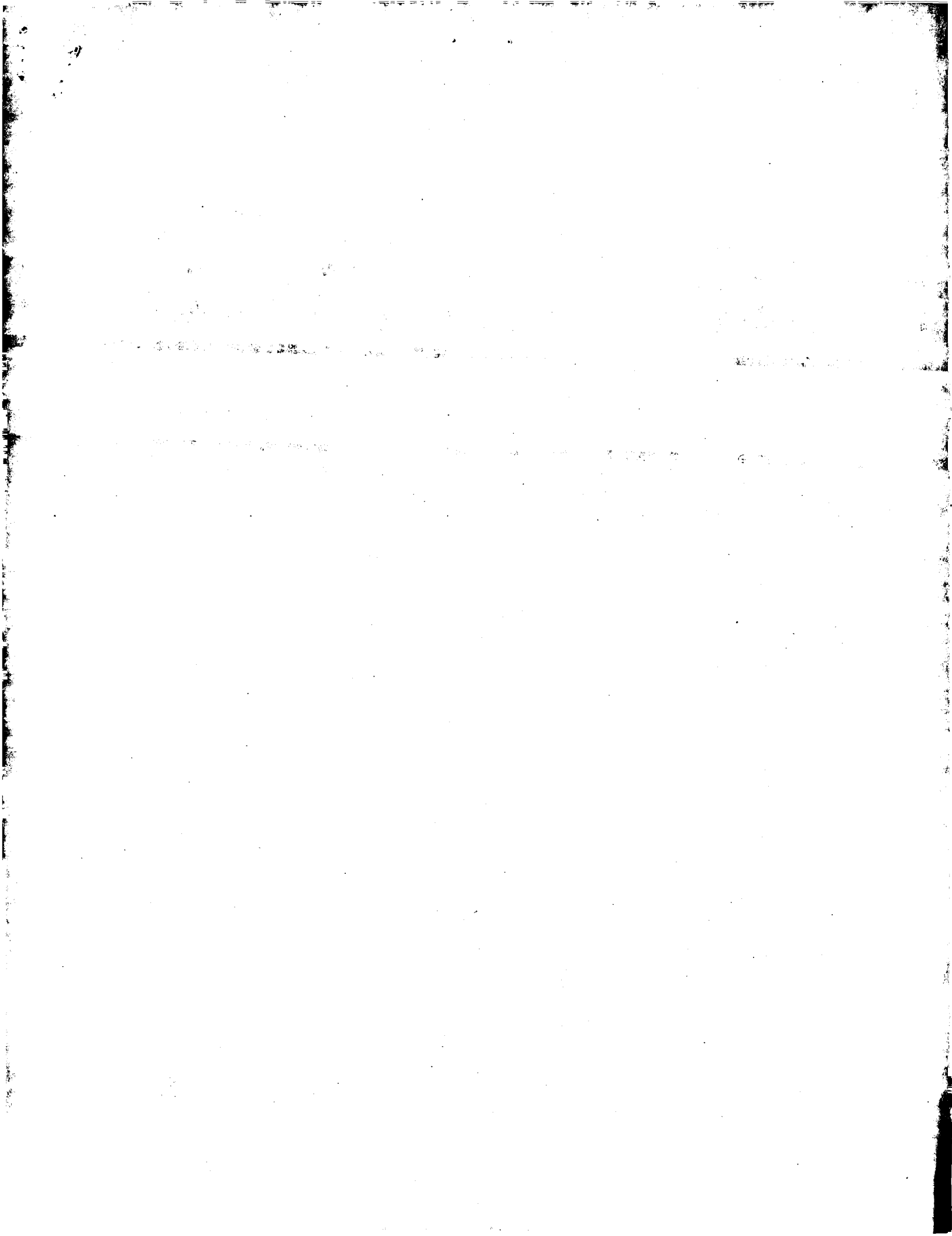
RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073750; AAL61413.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KM Receptor.

SO SEQUENCE 309 AA; 34586 MW; 7D9DADA3145BCAF9 CRC64;

Query Match

Best Local Similarity 57.0%; Score 918; DB 11; Length 309;
 Matches 167; Conservative 54; Mismatches 72; Indels 0; Gaps 0;

QY 9 VTEFVFLGTDNRVLEMLFPMASAIYMLTSGNIIITATVFTPSLHTPMYFPLSNLSF 68
 DB 9 VTEFVFLGTDNRVLEMLFPMASAIYMLTSGNIIITATVFTPSLHTPMYFPLSNLSF 68
 QY 7 VTEFVFLGTDNRVLEMLFPMASAIYMLTSGNIIITATVFTPSLHTPMYFPLSNLSF 66
 DB 7 VTEFVFLGTDNRVLEMLFPMASAIYMLTSGNIIITATVFTPSLHTPMYFPLSNLSF 66
 QY 69 IDCHSVTVPKMLBGLLERTISFNDCTQLFPLHACAEIFLLIIVAYDRYVAICT 128
 DB 69 IDCHSVTVPKMLBGLLERTISFNDCTQLFPLHACAEIFLLIIVAYDRYVAICT 128
 QY 67 VEICYSTAPKILDLIAEKKSISVWGMTQLFPMHFGGAEIFLLIIVAYDRYVAICT 126
 DB 67 VEICYSTAPKILDLIAEKKSISVWGMTQLFPMHFGGAEIFLLIIVAYDRYVAICT 126
 QY 129 PLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCDVPLVTLK 188
 DB 129 PLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCDVPLVTLK 188
 QY 127 PLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCDVPLVTLK 186
 DB 127 PLHYPNMMNRVCIOQVPMGLGTVHSGQTFLLTRLPYCGPNIIDSFFCDVPLVTLK 186



Query Match	Similarity	Score	DB	Length
Best Local Similarity	50.8%	Pred. No. 3.5e-56;		
Matches 153; Conservative	60;	Mismatches 88;	Indels 0;	Gaps 0;
DOMAIN	220	235	CYTOPLASMIC (POTENTIAL)	
FT TRANSMEM	236	258	6 (POTENTIAL)	
FT DOMAIN	259	269	EXTRACELLULAR (POTENTIAL)	
FT TRANSMEM	270	289	7 (POTENTIAL)	
FT DOMAIN	290	310	CYTOPLASMIC (POTENTIAL)	
FT DISULFID	97	189	BY SIMILARITY.	
FT CARBOHYD	5	5	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SEQUENCE	310 AA;	35358 MW;	076DCD28B16F70EC CRC64;	
Query Match	52.1%	Score 839;	DB 1;	Length 310;
Best Local Similarity	50.8%	Pred. No. 3.5e-56;		
Matches 153; Conservative	60;	Mismatches 88;	Indels 0;	Gaps 0;
1 MDLSNQFRTVEFVPLGLDNRVLELFPMASSAIYMLTSGNIIILIAITVETPESLHPMY	60			
1 MEPOQTIVSMVELFGFSQTELOKFLFLPLVLYVTIIVANLLMVTVTPDCRLHPMY	60			
61 FFLSLMSFIDICSHSSVTPKMLEGLLEKRTISFPNCITQPLFLHFACAEIFLLIIVAY	120			
61 FLRLRLAIDICSYTSTVSPKHLVDFLHETKTIISYGCMAQAFPHLLGGGVFLISWAY	120			
121 DRYAICTPLHYPNVMNRVCIQVLFALMLGTVHSLGQTEFLTRLPGCGNIIDSYFCD	180			
121 DRYIASQPLRVRTYIMTQLCVGLVAAMVGFSVSIQALMILPLPCDENIIDNFYCD	180			
181 VPLVIKACPTDTYLTGLIIVNMSGTISLSCFLAVTSTFWIILVSLRKHSAGRKALSTC	240			
181 VPOVRLRLACTPTSLIEFLMIFNSGLVLIWFLLIISTYVILVMLRSHSGARRRAASTC	240			
241 SAHFVAVLFPQPCFITYTRPDTSFSDIKVSVFVTVTPPLNPEITYLRNBEVSKAMKO	300			
241 TTHIIVSMIRFICLIYITWPTPTPLMKAVSISTVMTPLNPMIYITLRQDKAMMR	300			
301 L 301				
301 L 301				

KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 235 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 236 258 6 (POTENTIAL).
FT DOMAIN 259 269 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 270 289 7 (POTENTIAL).
FT DOMAIN 290 307 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 189 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 307 AA; 34958 MW; 5C8C68269034EBD3 CRC64;
Query Match 50.5%; Score 813.5; DB 1; Length 307;
Best Local Similarity 49.8%; Pred. No. 2.9e-54;
Matches 153; Conservative 63; Mismatches 90; Indels 1; Gaps 1;
QY 1 MDSLNQRYVEFYGLGTDNRVLEMLFFMAFSAYMLTSLGNLIILIAVFTPSLHPMY 60
DB 1 METSNLWVSDPVELGSQTRERLRFLEFLMFIFYITVWGNLIILITVSDSQLHPMY 60
QY 61 PFLNLSFIDCHSSVVPKMLEGLLEKRTISFDCNCTOLFPLHPACAEIFLLIIVAY 120
DB 61 FLNRLNLAVLDCESSVTPAPKMLVDLSEKRTISVSGCMGQIFPHPLGAMVFFLSYMAF 120
QY 121 DRYVAICTPLHPVPMNMRVCIOFLVFLMLGTVHSLGQFTFLRPLPYCGPNIIIDSYCD 180
DB 121 DRLAIIRPLKAYVTVMNTQOLWGLVAVATWGGFVHSLVQALMLPLPFCGPNIIDNPFCD 180
QY 181 VPLVIKACACTDTYTLGLIITNGSTISLSCFLAVVTSYMTILVSLRHSAGRKALSTC 240
DB 181 VPOVLRACDUTSLLEFLKISNSGLADVVMFFLLMSYLFLLVLRSHPGARRKAASTC 240
QY 241 SAHFVMAALFPGPCIFITYTPDPTFSIDKVVSVYVTVTPPLNPFITLNEEYKSAWKQ 300
DB 241 TTHIIVSMIFVPSIYLXAPRFPFPMDKLVISGHTYMTMLNPMIYTLANQDMAVVR 300
QY 301 L-ROROV 306
DB 301 LGRRLV 307
RESULT 3
ID QAF3_HUMAN STANDARD; PRT; 312 AA.
AC 095013;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 4F3.
GN OR4F3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Courtney L., Langston Y., Stoneking T., Drone K., Shih K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; AC004908; ADO5195.1; -
InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR000237; GPCRHOOPS.

DR PROSITE; PS00237; G-PROTEIN_RECEP_P1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_P1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).
FT TRANSMEM 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT TRANSMEM 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT TRANSMEM 220 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 258 6 (POTENTIAL).
FT DOMAIN 259 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 289 7 (POTENTIAL).
FT DOMAIN 290 312 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 189 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 312 AA; 35087 MW; ABEE3FAABA43F86 CRC64;

Query Match 48.5%; Score 781; DB 1; Length 312;
Best Local Similarity 45.8%; Pred. No. 7.9e-52; Indels 0; Gaps 0;
Matches 142; Conservative 71; Mismatches 97;

1 MDSLNQRTVEFVFLGLTDNRVLEMLFMAFSAIYMLTSGNIIIIATVFTPSLHTPMY 60
1 MDENHSVSEFLFLGTHSWEIOILLVSVLYVASINGNIIIVSVTTDPHLSPMY 60
61 FPLSNLSFIDICHSSTVTPKMLEGLLEKRTISFNCITQLPFLHFAEAFILIIIVAY 120
61 FLIASISFIDLGACSVTPMAYDLPRKRKIVFGGCIADIFRIHYIGVEMVLLIAMA 120
121 DRVVAICTPLAHYNNMNRVCIQVPAIMLGSTVHSLGQFTLIRPYCGPNIIISYPCD 180
121 DRVVALCKPLHLYTISPRKCLSFPLAVAMTIGVSHSLFQLAFLVNLAFGEPNVLDSFYCD 180
181 VPLVIACTDLYLTGLIVTNSGTSLSCELAIVTSYVAVLSLRKHSAGROKALSTC 240
181 LPLRLACTDLYLTGLIVTNSGTSLSCELAIVTSYVAVLSLRKHSAGROKALSTC 240
241 SAHFNVVALFFGFCIFLYTRPDTSFSI-DKVASVFTVVTPLNPLPIYTLRNEVSKA 300
241 SAHSTVALLFFGPMVETVRPHNSQMDKFLAFDAVLTPLNPLVYTFPKMKMAIKR 300
301 LRQGVFFTK 310
301 VCKQVVIYKR 310

RESULT 4
ID OSVL HUMAN STANDARD; PRT; 321 AA.
AC 09UGF6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 51, Last annotation update)
DE Olfactory receptor 5VL (Ha6M1-21).
OS OR5V1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid-9606;
[1]

SEQUENCE FROM N.A.

Tracey A.;

Submitted (DEC-1999) to the EMBL/Genbank/DDB databases.

-1- FUNCTION: PUTATIVE ODOANT RECEPTOR.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; AL096770; CAB65797.1; -

GeneW; HGNC.11972; OR5V1.

InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR000237; GPCRHOOPS.

DR PROSITE; PS00237; G-PROTEIN_RECEP_P1_1; 1.

DR PROSITE; PS50262; G-PROTEIN_RECEP_P1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).
FT TRANSMEM 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT TRANSMEM 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT TRANSMEM 220 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 292 7 (POTENTIAL).
FT DOMAIN 293 321 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 189 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 321 AA; 36056 MW; AAC426FDC58E375 CRC64;

Query Match 45.2%; Score 727.5; DB 1; Length 321;
Best Local Similarity 45.7%; Pred. No. 8.3e-48;
Matches 139; Conservative 67; Mismatches 95; Indels 3; Gaps 2;

1 MDSLNQRTVEFVFLGLTDNRVLEMLFMAFSAIYMLTSGNIIIIATVFTPSLHTPMY 60
1 MERKQOTATIEBIIILFSSNLELOPLFTIFLYTFTLGNIIILITVTDPHLTPMY 60
61 FPLSNLSFIDICHSSTVTPKMLEGLLEKRTISFNCITQLPFLHFAEAFILIIIVAY 120
61 YFLGNLAFIDICYTTNSVQVWVHLSKKKSIISYGVQVQALPAFPVGSCELLAAMV 120
121 DRVVAICTPLAHYNNMNRVCIQVPAIMLGSTVHSLGQFTLIRPYCGPNIIISYPCD 180
121 DRVVAICNPLRYSVLSKVLQVLAASCAVAFINSVHTVLTPLCPFGCNOQINVPFC 180
181 VPLVIACTDLYLTGLIVTNSGTSLSCELAIVTSYVAVLSLRKHSAGROKALST 239
181 IIPPLILSGNLSVNEALISLGVITGWPFCILVSYICIIITLRISSSGRRKAST 240
240 CSAHFNVVALFFGFCIFLYTRPDTSFSI--DKVASVFTVVTPLNPLPIYTLRNEVSKA 297
240 CASHALIVFLFGSAIFTVVRISYLSKQRLVSVLSVVTPLNPLPIYTLRNDIKSA 300
298 MKQL 301
301 VKTI 304

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EMBL; US6420; AAB01214.1; -

DR Genew; HGNC:8347; ORS11.

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHOOPS.

DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.

DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.

KM G-protein coupled receptor; Transmembrane; Glycoprotein;

KM Multigene family; Olfaction.

FT DOMAIN 1 28

FT TRANSMEM 29 51

FT DOMAIN 52 59

FT TRANSMEM 60 81

FT DOMAIN 82 102

FT TRANSMEM 103 122

FT DOMAIN 123 141

FT TRANSMEM 142 166

FT DOMAIN 167 207

FT TRANSMEM 208 228

FT DOMAIN 229 241

FT TRANSMEM 242 262

FT DOMAIN 263 273

FT TRANSMEM 274 294

FT DOMAIN 295 314

FT DISULFID 99 191

FT CARBOHYD 7 7

SC SEQUENCE 314 AA; 36048 MW; 334BB9BF3D9A4D63 CRC64; (POTENTIAL).

Query Match 43.1%; Score 694.5; DB 1; Length 314; Best Local Similarity 43.9%; Pred. No. 2.4e-45; Matches 134; Conservative 62; Mismatches 106; Indels 3; Gaps 2;

QY 5 NOTRTVEFVFLGLTDRVLEMLFPMASAIYMLTSGNLIITATVTFPSLHTPMYFPLS 64

DB 7 NTLVTEFILLGFPTRPELQIVLFVFLTVAILITGNIGMLINIDPHLOTPMFFLS 66

QY 65 NLSFDICHSVTPVKMGLLEKRTISPDCITQFLPHLPACAEIFLLIIVAYDRYV 124

DB 67 NLSFVDLCYFSDVPKMLVNFLESENKSIYGCALQFYFPCFPADTESFLLAMAYDRYV 126

QY 125 AICTPLHYPMVMNRVCIOVLPALMGVTHSGTFLIRLRYCGPNITDSFCVPLV 184

DB 127 AICNPFLIYVMSRGICMLRIIVSYLGAMNSLVHTSPAFILKYCDNVINHFCDPLP 186

QY 185 IKLACTDYLTGILIVTNSGTISLSCFLAVTSYVWILVLSLRK-HSABGRKALSTCSAH 243

DB 187 LKLSCTDTINEMLTSTYSSVEILCFIIIIISYFLLSVLKIRSPSGKKTFTSCAH 246

QY 244 FMVVALFPGPCITITRPTDSF--IDKVSVFYTVTPPLNPFYITLRNEEYKAMKQI 301

DB 247 LRSVITVIGTLLFIYSRPTLYSPNTDKIISVFYITFIPVLPNLIYSLRNKVDYDAERK 306

QY 302 ROROV 306

DB 307 LRSKV 311

RESULT 7

OLFL CANPA STANDARD; PRT; 311 AA.

AC 095154; DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 01-NOV-1997 (Rel. 35, Last annotation update)

OC Olfactory receptor-like protein OLFL.

OC Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Pisetipedia; Canidae; Canis.

OX NCBI_TaxId=9615;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=97008103; PubMed=8855279;

RX Isseel-Tarver L., Rine J.;

RA "Organization and expression of canine olfactory receptor genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:10897-10902(1996).

CC -1- FUNCTION: PUTATIVE ODOANT OR SPERM CELL RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; US3679; AAB37239.1; -

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHOOPS.

DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.

DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.

KM G-protein coupled receptor; Transmembrane; Glycoprotein;

KM Multigene family; Olfaction.

FT DOMAIN 1 24

FT TRANSMEM 25 48

FT DOMAIN 49 56

FT TRANSMEM 57 78

FT DOMAIN 79 99

FT TRANSMEM 100 119

FT DOMAIN 120 138

FT TRANSMEM 139 157

FT DOMAIN 158 195

FT TRANSMEM 196 218

FT TRANSMEM 219 235

FT TRANSMEM 236 259

FT DOMAIN 260 271

FT TRANSMEM 272 291

FT DOMAIN 292 311

FT CARBOHYD 4 4

SC SEQUENCE 311 AA; 35209 MW; 05A213247AF543A1 CRC64;

Query Match 43.0%; Score 693; DB 1; Length 311; Best Local Similarity 45.5%; Pred. No. 3.1e-45; Matches 138; Conservative 56; Mismatches 105; Indels 4; Gaps 3;

QY 1 MDSLNOTRTVEFVFLGLTDRVLEMLFPMASAIYMLTSGNLIITATVTFPSLHTPMY 60

DB 1 MGS-NTLVTEFILLGFPTRPELQIVLFVFLTVAILITGNIGMLIRTPHLOTPMY 59

QY 61 FPLSNLSFDICHSVTPVKMGLLEKRTISPDCITQFLPHLPACAEIFLLIIVAY 120

DB 60 FPLSNLSFDICHSVTPVKMGLLEKRTISPDCITQFLPHLPACAEIFLLIIVAY 119

QY 121 DRYVAICPLHYPMVMNRVCIOVLPALMGVTHSGTFLIRLRYCGPNITDSFCVPL 180

DB 120 DRYVALCNPLIYVMSRGICVWLIVLSTYIGAMNSLVHTSPAFILKYCDKVINHFCD 179

QY 181 VPLVIAKCTDYLTGILIVTNSGTISLSCFLAVTSYVWILVLS-LRKHSABGRKALST 239

DB 180 LPLPLKLSCTDTSVNMELMLSTYSSVEILCFIVIVISYFILLRSVLRIRSSGKKTFT 239

QY 240 CSAHEFVVALFPGPCITITRPTDSF--SIDKVSVFYTVTPPLNPFYITLRNEEYK 297

DB 240 CASHLTSVAIVGTTLLFIYSRPTLYSPNTDKIISVFYITFIPVLPNLIYSLRNKVD 299

QY 298 MKQ 300

DB 300 AKR 302

RESULT 8
OCD2_HUMAN STANDARD; PRT; 307 AA.
ID AC P58182; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN Olfactory receptor 12D2 (Hs6M1-20).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Uner M.M., Guillaudoux T., Vu Q., Kulyavin T., Harter H.,
RT Geraghty D.E.;
RL "Large scale sequence analysis of the human MHC class I region."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Whitaker H.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; AC004171; -; NOT ANNOTATED_CDS.
CC EMBL; AL035542; CAB44510.1; -.
CC DR Genew; HGNC:8178; OR12D2.
CC DR InterPro: IPR000276; GPCR_Rhodopsn.
CC DR Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR00237; GPCR_Rhodopsn.
CC DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; FALSE_NEG.
CC DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multi-gene family; Olfaction.
FT DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 24 47 1 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 48 55 2 (POTENTIAL).
FT TRANSSEM 56 77 2 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 78 98 3 (POTENTIAL).
FT TRANSSEM 99 118 3 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 119 137 4 (POTENTIAL).
FT TRANSSEM 138 156 4 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 157 193 5 (POTENTIAL).
FT TRANSSEM 194 217 5 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 218 235 6 (POTENTIAL).
FT TRANSSEM 236 258 6 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 259 271 7 (POTENTIAL).
FT TRANSSEM 272 291 7 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 292 307 7 BY SIMILARITY.
FT DISULFID 3 187 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 5 3 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 307 AA; 34872 MW; 76DDAC6CFF75C530 CRC64;

Query Match 42.8%; Score 689; DB 1; Length 307;
Best Local Similarity 43.9%; Pred. No. 6,1e-45;
Matches 134; Conservative 62; Mismatches 105; Indels 4; Gaps 2;

4 LNCRVTEFVFLGIDNRVLEMFMAFSATYMTLSGNIIITATVFTBSLHPMFFL 63
2 LNTTSVTEFLLGIDNRVLEMFMAFSATYMTLSGNIIITATVFTBSLHPMFFL 61

64 SNLSFIDCHSSVYVPMKLEGLLEKRTISFNCITQLEFLLHFAACAEILLIIVAYDXY 123
62 GNLSYDIDCYSTVTLTPKMLQNFSLTHKASIFSGICISQLHFFHFGSTESMLFAVMAFDLS 121
124 VAICTPLHAPNMMNRVCIQVPAFLMGTVSLGQTFITLTPYCGPIIISYPCDVL 183
122 VALCKPLRATVIMNPOLCTQMAITTWIGFFHALLHSVWTSRLNFCGSRHIFHFLCDIRP 181
184 VIKLACTDLYLGLILVTSNGTISLSCFLAVTVSYVIVLSL-RKHSAGROKALSTCS 241
182 LKLACAGNTEINOMLSTVGTITAMGFPLTILSYITTYLFPKRSQSMCKALSTCA 241
242 AHEMVVAFPFPGICITVTRP--DTSFSDIKVSVFVTVVTPPLNPFITLRNEEVKANK 299
242 SHEMVVILFYAPVLFYIHFALESFMDQDRIVAIMVTVVTPVLPNPLITLRNKEVGAIG 301
300 QLRQR 304
302 RVLR 306

RESULT 9
OCD2_HUMAN STANDARD; PRT; 308 AA.
ID AC Q9H210; Q95224;
DT 16-OCT-2001 (Rel. 40, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Olfactory receptor 2D2 (Olfactory receptor 11-610) (HB2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasios M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Traak B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395 (2001).
RN [2]
RP SEQUENCE OF 67-283 FROM N.A.
RX MEDLINE=99005533; PubMed=9787077;
RA Buettner J.A., Glusman G., Ben-Arie N., Ramos P., Lancet D.,
RA Evans G.A.;
RT "Organization and evolution of olfactory receptor genes on human
RT chromosome 11."
RL Genomics 53:56-68 (1998).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; AF321237; AAG45204.1; -.
CC EMBL; AF065876; AAC70020.1; -.
CC DR Genew; HGNC:8244; OR2D2.
CC DR GO; GO:0016021; C:Integral to membrane; NAS.
CC DR GO; GO:0004984; F:Olfactory receptor activity; NAS.
CC DR GO; GO:0007608; P:Olfaction; NAS.
CC DR InterPro: IPR000276; GPCR_Rhodopsn.
CC DR Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR00237; GPCR_Rhodopsn.
CC DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; FALSE_NEG.
CC DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.

KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSSEM 26 49
 FT TRANSSEM 50 57
 FT TRANSSEM 58 79
 FT TRANSSEM 80 100
 FT TRANSSEM 101 120
 FT TRANSSEM 121 139
 FT TRANSSEM 140 158
 FT TRANSSEM 159 195
 FT TRANSSEM 196 219
 FT TRANSSEM 220 236
 FT TRANSSEM 237 259
 FT TRANSSEM 260 270
 FT TRANSSEM 271 290
 FT TRANSSEM 291 308
 FT CARBOHYD 5
 FT CONFLICT 134
 FT SEQUENCE 308 AA; 34130 MM; 0651A5973426082A CRC64;
 Query Match 42.6%; Score 686.5; DB 1; Length 308;
 Best Local Similarity 43.4%; Pred. No. 9.5e-45;
 Matches 135; Conservative 58; Mismatches 105; Indels 13; Gaps 2;
 QY 1 MDSLNQTRVTEFVFLGLTDNRVLEMLFPMASAIYMLTSGNLIILIAVFTPSLHTPMY 60
 1 MRQINQVTEFLLGLSDPHRQLFLVGLVLTAVTANLILSLVAVDSQLHTPMY 60
 QY 61 PFLSNLSFDICHSSTVPKMLEGLLEKRTISFNCITQLFPLHFACAEFLLIYAY 120
 61 PFLCNLSLADLCFSTINIPQALVHLSRKKVIAFTLCANLFLFLGCTGCALLVMSY 120
 QY 121 DRVVAICTPLHYPNVMNRVCIOVFLMIGTVHSGQETLIRLPYCGPIIDSYFCD 180
 121 DRVVAICNPRLPYDIPMTWKVCVQLAGSWTSGLVSVVDFTLRLPYRGSNSIAHFCE 180
 QY 181 VPLVIKLACTDT-----YLTLGLIVNSGTISLSCFLAVTSYVILVSRKHSAGR 233
 181 APALLILASTDTTASAMAILTLTGVI-----LLIPFLILVSGRIYIVVVMKSTVGS 234
 QY 234 QKALSTCSAHFNVVALFPGPCIFLYTRPDTSFSDKVSVFYVTVPLNPLPIYTLRNEE 293
 235 LKAFSTCGSHLMVVIIFYGSAIITYMTPKSKKOEKSVSFVAIVTPEMLPLIYSIRNKO 294
 QY 294 VKSAMKQLROR 304
 295 VKALKRKVATR 305
 DB
 RESULT 10
 OLFS RAT STANDARD; PRT; 313 AA.
 ID AC P3326;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Olfactory receptor-like protein F5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91191556; Pubmed=1840504;
 RA Buck L.; Axel R.;
 RT "A novel multigene family may encode odorant receptors: a molecular
 basis for odor recognition."
 RC Cell 65:175-187(1991).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIAL.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 DR EMBL; M64377; AAA41740.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECPT_P1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSSEM 26 50
 FT TRANSSEM 51 57
 FT TRANSSEM 58 79
 FT TRANSSEM 80 100
 FT TRANSSEM 101 120
 FT TRANSSEM 121 139
 FT TRANSSEM 140 158
 FT TRANSSEM 159 196
 FT TRANSSEM 197 219
 FT TRANSSEM 220 236
 FT TRANSSEM 237 260
 FT TRANSSEM 261 272
 FT TRANSSEM 273 292
 FT TRANSSEM 293 313
 FT CARBOHYD 5
 FT DISULFID 97
 FT SEQUENCE 313 AA; 34703 MM; 2FD7BCD6B3D6815 CRC64;
 Query Match 42.6%; Score 686.5; DB 1; Length 313;
 Best Local Similarity 43.8%; Pred. No. 9.6e-45;
 Matches 133; Conservative 63; Mismatches 105; Indels 3; Gaps 2;
 QY 1 MDSLNQTRVTEFVFLGLTDNRVLEMLFPMASAIYMLTSGNLIILIAVFTPSLHTPMY 60
 1 MSTNQSSTVTEFLLGLSDPHRQLFLVGLVLTAVTANLILSLVAVDSQLHTPMY 60
 QY 61 PFLSNLSFDICHSSTVPKMLEGLLEKRTISFNCITQLFPLHFACAEFLLIYAY 120
 61 PFLSNLSFDVDFSSSTVPKLIANHLISQALISFGCLTQLFLAVFGMDNFLAVMSY 120
 QY 121 DRVVAICTPLHYPNVMNRVCIOVFLMIGTVHSGQETLIRLPYCGPIIDSYFCD 180
 121 DRVVAICNPRLPYDIPMTWKVCVQLAGSWTSGLVSVVDFTLRLPYRGSNSIAHFCE 180
 QY 181 VPLVIKLACTDTYLGLILVNSGTISLSCFLAVTSYVILVSRKHSAGR 233
 181 GTPPLKSCSDTHLMLITLGAIVVWTPFCILISYHILCAVLRVSSPGKWKSFST 240
 QY 240 CSAHFNVVALFPGPCIFLYTRPDTSF--SIDKVSVFYVTVPLNPLPIYTLRNEVSA 297
 241 CGSHLAVVCLFYGTIVIAVFNSSSHLAGRDMAAVTAIVTPEMLPLIYSIRNSDMKAA 300
 QY 298 MKQL 301
 301 LKRV 304
 DB
 RESULT 11
 OAC1 HUMAN STANDARD; PRT; 312 AA.
 ID AC Q96KKA;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Olfactory receptor 10C1 (Hs6M1-17).

GN OR10C1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Whitaker H.;
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: AL035542; CAB44507.1; ALT INIT.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 24
 FT TRANSSEM 25 48
 FT TRANSSEM 49 56
 FT TRANSSEM 57 78
 FT DOMAIN 79 99
 FT TRANSSEM 100 119
 FT TRANSSEM 120 138
 FT TRANSSEM 139 157
 FT TRANSSEM 158 194
 FT TRANSSEM 195 218
 FT TRANSSEM 219 235
 FT TRANSSEM 236 258
 FT DOMAIN 259 271
 FT TRANSSEM 272 291
 FT DOMAIN 292 312
 FT DISULFID 96 188
 FT CARBOHYD 4 4
 SQ SEQUENCE 312 AA; 34351 MM; B6PDE0E700CB2CC CRC64;
 Query Match 42.3%; Score 681.5; DB 1; Length 312;
 Best Local Similarity 45.6%; Pred. No. 2.3e-44;
 Matches 140; Conservative 55; Mismatches 109; Indels 3; Gaps 2;
 Db 302 RRIQKT 308
 RESULT 12
 ID OCDS_HUMAN STANDARD; PRT; 316 AA.
 AC 09UGF7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Olfactory receptor 12D3 (Hs6M1-27).
 GN OR12D3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Testis;
 RA Volz A., Ehlers A., Younger R., Forbes S., Trowdale J., Beck S.,
 RA Ziegler A.;
 RT "Complex transcriptional control of MHC-linked olfactory receptor
 RT genes includes long distance and extensive alternative splicing, exon
 RT splicing and premature polyadenylation."
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Tracey A.; (DEC-1999) to the EMBL/Genbank/DBJ databases.
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ459858; CAD31041.1; -;
 DR EMBL: AL096770; CAB65796.1; -;
 DR Genew: HGNC:13963; OR12D3.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 23
 FT TRANSSEM 24 47
 FT TRANSSEM 48 55
 FT TRANSSEM 56 77
 FT TRANSSEM 78 98
 FT TRANSSEM 99 118
 FT TRANSSEM 119 137
 FT TRANSSEM 138 156
 FT TRANSSEM 157 193
 FT TRANSSEM 194 219
 FT TRANSSEM 220 235
 FT TRANSSEM 236 258
 FT TRANSSEM 259 271
 FT TRANSSEM 272 291
 FT TRANSSEM 292 316
 FT DISULFID 95 187
 FT CARBOHYD 3 3
 SQ SEQUENCE 316 AA; 35791 MM; 07FDCP869D898B2 CRC64;
 Query Match 42.3%; Score 681; DB 1; Length 316;
 Best Local Similarity 44.6%; Pred. No. 2.5e-44;

Db 302 RRIQKT 308
 RESULT 12
 ID OCDS_HUMAN STANDARD; PRT; 316 AA.
 AC 09UGF7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Olfactory receptor 12D3 (Hs6M1-27).
 GN OR12D3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Testis;
 RA Volz A., Ehlers A., Younger R., Forbes S., Trowdale J., Beck S.,
 RA Ziegler A.;
 RT "Complex transcriptional control of MHC-linked olfactory receptor
 RT genes includes long distance and extensive alternative splicing, exon
 RT splicing and premature polyadenylation."
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Tracey A.; (DEC-1999) to the EMBL/Genbank/DBJ databases.
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ459858; CAD31041.1; -;
 DR EMBL: AL096770; CAB65796.1; -;
 DR Genew: HGNC:13963; OR12D3.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 23
 FT TRANSSEM 24 47
 FT TRANSSEM 48 55
 FT TRANSSEM 56 77
 FT TRANSSEM 78 98
 FT TRANSSEM 99 118
 FT TRANSSEM 119 137
 FT TRANSSEM 138 156
 FT TRANSSEM 157 193
 FT TRANSSEM 194 219
 FT TRANSSEM 220 235
 FT TRANSSEM 236 258
 FT TRANSSEM 259 271
 FT TRANSSEM 272 291
 FT TRANSSEM 292 316
 FT DISULFID 95 187
 FT CARBOHYD 3 3
 SQ SEQUENCE 316 AA; 35791 MM; 07FDCP869D898B2 CRC64;
 Query Match 42.3%; Score 681; DB 1; Length 316;
 Best Local Similarity 44.6%; Pred. No. 2.5e-44;

Matches 137; Conservative 60; Mismatches 106; Indels 4; Gaps 2;

QY 5 NOTRVTEFVLGLTDRVLEMLFMAFSAIYMLTSGNIIIIATVTPSLHTPMYFPLS 64
 DB 3 NNTVTEFVLGLTDRVLEMLFMAFSAIYMLTSGNIIIIATVTPSLHTPMYFPLS 62
 QY 65 NLSFIDICHSVTVPMKLEGLLEKRTISPDNCITQLFPLHFAACAFILIIIVAYDRYV 124
 DB 63 NLSGLDTSYSSVTLKLVNLCVSRRAISPLGCTQTHFHLFGLSTAILIIMAFDRYV 122
 QY 125 AICTPLHYPMVMNRVCIQVFLALMIGTVAHSGQTFILTRPYCGNIIDSYFCDVPLV 184
 DB 123 AICPLHYTYIMNPQVCIILAAAMLIISFYALMHSVMTAHLSPGSGQKLNHFYDVXPL 182
 QY 185 IKLACTDTYLTGLIIVTNSGTSISLSCFLAVTS--IVVILVSLKSKHAEGRKALSTCSA 242
 DB 183 LELACSTLTNLQMLISTVTSISISMGAFITLLSCFYIYIGLFPNRCRIIHLALSTCSA 242
 QY 243 HFVVALFEGPCIFITYRPTDSFSL--DKVSVFYVTVFELNPFITLNEEYKSAKQ 300
 DB 243 HFVVALFEGPCIFITYRPTDSFSL--DKVSVFYVTVFELNPFITLNEEYKSAKQ 300
 QY 301 LRORQVF 307
 DB 303 IFGRKLF 309

RESULT 13

OSBG_HUMAN STANDARD; PRT; 314 AA.

AC Q96R08;
 DT 26-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Olfactory receptor 5B16.
 GN O5B16.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE OF 66-281 FROM N.A.
 RA Fuchs T., Molecova B., Linhart C., Sharan R., Khen M., Herwig R.,
 RA Simulovich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
 RA Leirsch H., Olander Z., Guesman G., Lancelot D., Shantir R.;
 RT DEPOG: a practical scheme for deciphering families of genes.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: A939637; AK95122.1;
 CC InterPro: IPR000276; GPCR_Rhodopn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein-coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 24 47 1 (POTENTIAL).
 FT TRANSMEM 48 55 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 56 77 2 (POTENTIAL).
 FT DOMAIN 78 98 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 99 118 3 (POTENTIAL).
 FT DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 138 156 4 (POTENTIAL).
 FT DOMAIN 157 193 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 194 217 5 (POTENTIAL).
 FT DOMAIN 218 234 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 235 257 6 (POTENTIAL).
 FT DOMAIN 258 270 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 271 290 7 (POTENTIAL).
 FT DOMAIN 291 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 291 314 BY SIMILARITY.
 FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 314 AA; 35181 MW; 93BB84FLCACA68F1 CRC64;

Query Match 42.1%; Score 677.5; DB 1; Length 314;
 Best Local Similarity 44.1%; Pred. No. 4,6e-44;
 Matches 132; Conservative 58; Mismatches 106; Indels 3; Gaps 2;

QY 5 NOTRVTEFVLGLTDRVLEMLFMAFSAIYMLTSGNIIIIATVTPSLHTPMYFPLS 64
 DB 3 NNTVTEFVLGLTDRVLEMLFMAFSAIYMLTSGNIIIIATVTPSLHTPMYFPLS 62
 QY 65 NLSFIDICHSVTVPMKLEGLLEKRTISPDNCITQLFPLHFAACAFILIIIVAYDRYV 124
 DB 63 NLSGLDTSYSSVTLKLVNLCVSRRAISPLGCTQTHFHLFGLSTAILIIMAFDRYV 122
 QY 125 AICTPLHYPMVMNRVCIQVFLALMIGTVAHSGQTFILTRPYCGNIIDSYFCDVPLV 184
 DB 123 AICPLHYTYIMNPQVCIILAAAMLIISFYALMHSVMTAHLSPGSGQKLNHFYDVXPL 182
 QY 185 IKLACTDTYLTGLIIVTNSGTSISLSCFLAVTS--IVVILVSLKSKHAEGRKALSTCSA 243
 DB 183 LELACSTLTNLQMLISTVTSISISMGAFITLLSCFYIYIGLFPNRCRIIHLALSTCSA 242
 QY 243 HFVVALFEGPCIFITYRPTDSFSL--DKVSVFYVTVFELNPFITLNEEYKSAKQ 300
 DB 243 HFVVALFEGPCIFITYRPTDSFSL--DKVSVFYVTVFELNPFITLNEEYKSAKQ 300
 QY 244 LFVAVSIFGTGIFMYLPRNSHFMGTDMASVFAIVLPMPLVYSLNKEVKSFAFK 301

RESULT 14

07C1_HUMAN STANDARD; PRT; 320 AA.

AC Q76099; Q15621;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Olfactory receptor 7C1 (Olfactory receptor 7PC86).
 GN OR7C1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA TISSUE=Septm;
 RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
 RA Burkhardt-Schultz R.J., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala M., Terry A., Garmes J.,
 RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
 RA Liu S., Altix C., Andreise T., Frankheim M., Amico-Keller G.,
 RA Coetfield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Krommiller B., Arellano A., Montgomey M., Ow D., Nolan M., Trong S.,
 RA Kobayashi A., Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of an ~1.5 Mb olfactory receptor (OLFR) cluster in
 RT 19q13.1";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE OF 126-282 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97224452; PubMed=9119360;
 RA Vassart G., Parmentier M.;
 RT "Specific repertoire of olfactory receptor genes in the male germ
 RT cells of several mammalian species";
 RL Genomics 39:239-246 (1997).

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; AC005255; AAC25625.1; -
 DR EMBL; X89676; CAA61823.1; -
 DR PIR; S58004; S58004.
 DR Genew; HGNC:8373; OR7C1.
 DR GO; GO:0007283; P:physiological processes; TAS.
 DR GO; GO:0007283; P:spermatogenesis; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 196 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 197 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 237 259 6 (POTENTIAL).
 FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 313 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 314 333 BY SIMILARITY.
 FT DISULFID 97 189 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 5 5 E -> K (IN REF. 2).
 FT CONFLICT 171 171 E -> P (IN REF. 2).
 FT CONFLICT 210 210 V -> L (IN REF. 2).
 FT CONFLICT 247 247
 SQ SEQUENCE 320 AA; 35518 MW; BBDCC409721D70C4 CRC64;
 Query Match 42.0%; Score 676.5; DB 1; Length 320;
 Best Local Similarity 42.1%; Pred. No. 5.5e-44;
 Matches 134; Conservative 64; Mismatches 113; Indels 7; Gaps 3;

DB 299 RALGRLSRATFENGDT 316
 RESULT 15
 ID OIQ1_HUMAN STANDARD; PRT; 314 AA.
 AC Q15612;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 101 (Olfactory receptor TFCR106) (Olfactory
 DE receptor 9-A) (OR9-A).
 GN Orl1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE OF 126-282 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97224452; PubMed=9119360;
 RA Vanderhaeghen P., Schumans S., Vassart G., Parmentier M.;
 RT "Specific repertoire of olfactory receptor genes in the male germ
 RL cells of several mammalian species.";
 RL Genomics 39:239-246 (1997).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; X89676; CAA61814.1; -
 DR PIR; S58012; S58012.
 DR Genew; HGNC:8223; OR101.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0004984; F:olfactory receptor activity; NAS.
 DR GO; GO:0007608; P:olfaction; NAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 196 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 197 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 237 259 6 (POTENTIAL).
 FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 314 BY SIMILARITY.
 FT DISULFID 97 189 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 5 5 I -> F (IN REF. 1).
 FT CONFLICT 126 126
 SQ SEQUENCE 314 AA; 35615 MW; 50DOAB08946B4EFC CRC64;
 Query Match 41.9%; Score 675; DB 1; Length 314;
 Best Local Similarity 43.8%; Pred. No. 7e-44;
 Matches 137; Conservative 64; Mismatches 106; Indels 6; Gaps 5;

Qy 1 MDSINOTRTEFEVFLGTDNRVLEMLPFMAFSAIYMLTUSGNILIIATVFTDSLHTPMY 60
 Db 1 MDNSNMTSVSHFVLGISTHBEQIPLFVPSLMTAINISGNLAITTLISAPRLHTPMY 60
 Qy 61 FPLSNLSFIDICHSSVTPPKMLEGLLEKRTISFDCITQLFPLHLPACAEIFLLIIVAY 120
 Db 61 IFLSNLALTDICFTSTVPKMLQIIFSPTKVISYTGCLAQIYFPCFAMENFIIVMAY 120
 Qy 121 DRYVAICTPLHYPNVMMARVCIOLVFALMLGCTVHSLGOTFELTIRLPYCGPNIIIDSYECD 180
 Db 121 DRYVAICTPLHYPNVMMARVCIOLVFALMLGCTVHSLGOTFELTIRLPYCGPNIIIDSYECD 180
 Qy 181 VPLVIACTDVTYLTGILIVTNSGTISLSCFLAVVT-SY-WVILVSLRKHSAEGROKALS 238
 Db 181 LVYALMKISCTSTYNTLMHT-EGAVVISGALAFITASYACIILVLRIPSAGRWKTF 239
 Qy 239 TCSAHFNVALFPGPCIFITRPDPTSPSIDK--VVSVPYTVVTPPLNPFITYTLRNEBVS 296
 Db 240 TCGSHLTVAIFPGTLSMVYFRPLSSYSYTKGRITIVVTVVTPMLNPFITYSLRNGDVKG 299
 Qy 297 A-MKQLROROVPF 308
 Db 300 GFMKMSRMQTFP 312

Search completed: August 12, 2003, 16:07:15
 Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:01:51 ; Search time 39 Seconds

(without alignments)
771.815 Million cell updates/sec

Title: US-09-807-132-4

Perfect score: 1611

Sequence: 1 MDSLNQTRVTEPFVFLGUTDN.....VKSAMQLRQROVFPFKSYT 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_76:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	822	51.0	307	2	S29710
2	731	45.4	318	2	JCS202
3	680.5	42.2	313	2	B23701
4	674.5	41.9	333	2	A23701
5	661.5	41.1	310	2	B23701
6	660	41.0	327	2	F23701
7	659.5	40.9	312	2	A46247
8	658.5	40.9	314	2	H23701
9	657.5	40.8	309	1	S51356
10	656	40.7	314	2	S20572
11	656	40.7	314	2	A37286
12	655	40.7	313	2	S20571
13	653.5	40.6	312	2	I23701
14	645	40.0	305	2	S29711
15	644.5	40.0	311	2	JCS200
16	644.5	40.0	311	2	JCS200
17	644.5	40.0	319	2	S29707
18	643.5	39.9	312	2	JCS624
19	638.5	39.6	312	2	S29708
20	616	38.2	315	2	JCS536
21	615.5	38.2	304	2	S29709
22	602	37.4	315	2	JCS458
23	602	37.4	317	2	D23701
24	600	37.2	312	2	A48413
25	593.5	36.8	315	2	JCS201
26	586.5	36.4	316	2	A57069
27	555	34.5	320	2	S20573
28	554.5	34.4	311	2	C23701
29	530.5	32.9	312	2	A46750

30	471.5	29.3	224	2	S29000	G protein-coupled
31	466.5	29.0	264	2	PC4369	olfactory receptor
32	453	28.1	154	2	S58052	probable olfactory
33	452.5	28.1	321	2	H45774	odorant receptor 3
34	451.5	28.0	222	2	B40745	odorant receptor (
35	451	28.0	143	2	S58071	probable olfactory
36	443	27.5	143	2	S58006	probable olfactory
37	437	27.1	154	2	S58015	probable olfactory
38	436.5	27.1	216	2	I38474	olfactory receptor
39	432.5	26.8	216	2	I38474	olfactory receptor
40	428	26.6	225	2	I38478	olfactory receptor
41	427.5	26.5	222	2	D40745	odorant receptor (
42	426.5	26.5	216	2	I38470	odorant receptor (
43	426.5	26.5	222	2	C40745	odorant receptor (
44	419.5	26.0	232	2	S29001	G protein-coupled
45	419	26.0	328	2	G45774	odorant receptor 2

ALIGNMENTS

RESULT 1

S29710

olfactory receptor OR18 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998

C/Accession: S29710

R/Ramling, K.; Krueger, J.; Strotmann, J.; Boehhoff, I.; Kubick, S.; Baumstark, C.; Bree

Nature 361, 353-356, 1993

A/Title: Cloning and expression of odorant receptors.

A/Reference number: S29707, PMID:93149273; PMID:7678922

A/Accession: S29710

A/Molecule type: mRNA

A/Residues: 1-307 <RAM>

C/Superfamily: olfactory receptor OR14

Query Match 51.0%; Score 822; DB 2; Length 307;

Best local Similarity 51.2%; Pred. No. 2.1e-63; Matches 150; Conservative 55; Mismatches 88; Indels 0; Gaps 0;

QY	9	VTEFVPLGLDNRVLEMLPFMAFSALYMLTSGNLIILATVPTPSLHPTMVFSLNLSF	68
DB	7	ITREFILGLTOPDGRKALFVIFPLIYIVTMGNLIVTVLASPSLSPMFLASLTL	66
QY	69	IDICSSVTPPKMLBGLLERTKISPDNCITQFLHLPACBIFLLIIVAYDRYVACT	128
DB	67	LNALFSTALSPKLIADLYDOKTISFRACMSQLFTEHLFGVDIVLVMAAYDRVVAICK	126
QY	129	PLHYPMVMNRVCIQVFLMWIGTVSLGOTFLTRLPYCGPNITDSYFCVPLVIKLA	188
DB	127	PLHYLAIMNRVCIITLITAMTGGFTHSLIQVFPVYNLPFCGPNVIDHETCDMSPLVLVA	186
QY	189	CTDYVLTGILIVTNGSTISLSCFLAVTSSYVILVSLRHSABGRKALSTCSAHMVYA	248
DB	187	CTDYVLTGILVANGGVNCIVIFTLTSGYIILSLKTQSGEGRKALSTCSSHLVVI	246
QY	249	LRFGPCIFLYTPDPSFSDKVVSVFYTVVPLNPFITLNNBYKSAAMKOL	301
DB	247	LRFPICIFMYARPVNFPIDKCIIVFYITITMLNPLIYTLNNSIKSCMKXL	299

RESULT 2

JCS202

Chemoreceptor TR641 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999

C/Accession: JCS202; PC4304

R/Thomas, M.B.; Haines, S.L.; Akesson, R.A.

Gene 178, 1-5, 1996

A/Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.

A/Reference number: JCS200; PMID:97080538; PMID:8921883

A/Accession: JCS202

A/Status: preliminary; nucleic acid sequence not shown

A: Molecule type: DNA
A: Residues: 1-318 <TH01>
A: Cross-references: GB:U50949; NID:G1256392; P1DN:AAC52911.1; PID:G1256393
A: Accession: PC4304
A: Status: preliminary
A: Molecule type: protein
A: Residues: 145-153:245-253 <TH02>
A: Experimental source: taste bud
C: Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction.
C: Genetics:
A: Gene: tb641
C: Superfamily: olfactory receptor OR14
C: Keywords: olfaction; taste bud; transmembrane protein
F: 30-53/Domain: transmembrane #status predicted <TM1>
F: 63-84/Domain: transmembrane #status predicted <TM2>
F: 106-155/Domain: transmembrane #status predicted <TM3>
F: 145-159/Domain: transmembrane #status predicted <TM4>
F: 202-224/Domain: transmembrane #status predicted <TM5>
F: 243-255/Domain: transmembrane #status predicted <TM6>
F: 276-286/Domain: transmembrane #status predicted <TM7>

Query Match	45.4%;	Score 731;	DB 2;	Length 318;
Best Local Similarity	46.6%;	Pred. No. 1.5e-55;		
Matches 139;	Conservative 54;	Mismatches 103;	Indels 2;	Gaps 2;

OY	7	RVEFEVFGLDNRNLEMLPFMAFSALMYLTSNGIIILITVFPSPSLHT-PMYFELSN	65
Dd	11	TVDTEFLIGLANHPRLRKFELFLVFLIYLITQLSULLILLTYWADPKLHARMYLLGEV	70
OY	66	LSFDICHSSTVPKMLEGILLERKTISPDNCITQLPPLHLFACAEIFLLIIVAYDRYA	125
Dd	71	LSFLMMLSSVIPRIILINFPTANKRAIAFGCGCAQOLFFPHFGISTCPLYTTMAADRYDA	130
OY	126	ICTPLHPYVMAMRVCIOLVPAIMLGATVSHSGQTFELTRLPFCGNINIDSYPCDVPLVI	185
Dd	131	ICOPLRYPVLMMGKCTIIVAGAMVAGSIHGSIQALITRLRPFGCKEVDYFFCDIPAVU	190
OY	186	KLACTDYLYTGILLVTNSGTLSLSCFLAVTVTSMYLVLSLR-HSAEGRKALSTCSAHF	244
Dd	191	RLACADTAINELEVTFEDIGVVAASCELIILSTANIVHAALKIRKTADGGRRRAFSTCGSHL	250
OY	245	MVVALFEGGCITFYRRPDFSFSDIKVSYFYYVYVPLNPFTYTLLENBEVKASMQR	302
Dd	251	TVVTVYVVCITYLEPAGSKSSPDGANVAFFYVTVVPLNLPLTYLTNNQEVNSALKKL	308

RESULT 3

C:Olfactory receptor F5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C:Accession: B23701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A>Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556; PMID:1840504
A:Accession: B23701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-313 <BUC>
A:Cross-references: GB:M64377
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	42.2%;	Score 680.5;	DB 2;	Length 313;
Best Local Similarity	43.4%;	Pred. No. 3.3e-51;		
Matches 132;	Conservative 63;	Mismatches 106;	Indels 3;	Gaps 2;

```

Qy 1 MSLAQTPTPEVFLGJTDNRVLKEMLPFAFSAIYMLTSGNLIITAIYVTFPSLTPMY 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MSTTSSSTPEFLGJSRQPOQQQLFLFLIMLYATVGNLIITLALGTSRRTPMY 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 FELSNI+FDICHSSTVPRKLEGGLLERKTSIFDNCITQLPFLHLPA+CEIFLLIIVAY 120

```

Db 61 FFLSNLSFVDVCESSFTVPEKVLANIILISQAISSFGSCITQLYFLAVFGNMDNFLIAMSYS 120
 Qy 121 DRVVALCFEPLAHYENWNNNRVCYOLVFAELMLGGTSHSGQFELTRLPYCGNIIIDSYFCD 180
 Db 121 DRVVALCFEPLAHYTKTRTROLCVLLVSGSVVVAANNCLHILMLARKSFCDNMIPHFCD 180
 Qy 181 VPLVILACTDITYLIGLILVINSGTISLSCPLAVVTSYMLIVLS-LKHSABEQKALST 239
 Db 181 GTPLATKLSOSDRLHLEMLITGEAVVMVTPFVCLILSYIHITCIVLVSSPRGQWKSFT 240
 Qy 240 CSAHFVWVLLFFGCPICFIYTRBDTSF--SIRKVVSVFPTVTPPLNPFITYLRNBEVYKSA 297
 Db 241 CSHLAVVCLFGYIVAAVYFNPSSSHLAGRDMAAAVMVAVYTPMLNPFITYLSRNSDWKAA 300
 Qy 298 MKQL 301
 Db 301 LRRV 304

RESULT 4

Olfactory receptor F3 - rat
 C|Species: Rattus norvegicus (Norway rat)
 C|Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C|Accession: A23701
 R|Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A|Title: A novel multigene family may encode odorant receptors: a molecular basis for o
 A|Reference number: A23701, MUID:91191556, PMID:1840504
 A|Accession: A23701
 A|Status: nucleic acid sequence not shown
 A|Molecule type: mRNA
 A|Residues: 1-133 <BUC>
 A|CrossB-references: GB:M64376; NID:g205813; PIDN:AAA41739.1; PID:g205814
 C|Superfamily: Olfactory receptor OR14
 C|Keywords: G protein-coupled receptor; transmembrane protein

Query Match	41.9%	Score 674.5	DB 2	Length 333
Best Local Similarity	43.9%	Pred. 1.1e-50		
Matches 133; Conservative	62;	Mismatches 105;	Indels 3;	Gaps 2;

Oy	I	MSLSNTRVTEPEFGLIDNRVLBMLFEMABSAIYMLTSLGNILIIIAATVTPBSLHPMY	60
Db	1	MDSSNTRVSEFELLAGFVENKLOPLIYGLFSLMLTVIVNISIIYAIIISDPCLHPMY	60
Oy	61	FFLSNLSFSDICSSAVTEPOMLEGLLEBKRTISPNOCITOLEFHLFACAEIPLLIYAY	120
Db	61	FFLSNLSFSDICISTVPEKMLVNIQTQNNVITTAGCITQYFFLLFVELDNFLITIMAY	120
Oy	121	DRVVAICTPLHYPENVMANRVCITQVFAALMGTVASLGQTEFLTRLPYCGENIIIDSYFCD	180
Db	121	DRVVAICHPMHVIVIMNYRLCGFLVLSKNIVSVLHALQSLMLMLALPPTCHLELPHYFCE	180
Oy	181	VPLVIAKLACTDYLVGILIVTNSGTSLSCEFLAVTSYMIIVSL-RKHSAEGRQKALST	233
Db	181	PNQVITQLTCSDAFLNDLVITFVLVLAATVLAGIIFYSYFKIVSSICALISSVHGKYKAFST	240
Oy	240	CSAHFNVVALFF--GPCIFITTRPDTSPSIDKVSVEFTVOTPLNPIITVTLRMBEYKSA	297
Db	241	CASHLSVSLSFYCTGLGVYLSAANNSQASATASVMTVVTVMVNPETYSILRKMDYKSV	300
Oy	298	MKQ 300	
Db	301	LKK 303	

RESULT

01factory receptor I3 - rat
 C1Species: Rattus norvegicus (Norway rat)
 C1Date: 22-Jan-1993 #sequence_revision 22-Jan-1993
 C1Accession: E23701

R/Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A>Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556; PMID:1840504
A:Accession: E23701
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-310 <BUC>
A:Cross-references: GB:M64385; NID:g205831; PIDN:AAA41748.1; PID:g205832
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 41.1%; Score 661.5; DB 2; Length 310;
Best Local Similarity 43.4%; Pred. No. 1.4e-49;
Matches 129; Conservative 64; Mismatches 101; Indels 3; Gaps 2;

QY 5 NQRTVEFVFLGLTDNRVLEMLPFMAFSAIYMLTSGNIIIIATVTPSLHTPMYFELS 64
DB 3 NQRTVQFLGLGPIPEHQHLEFVALVVMYLTIIIGNLIIIVLVQDSQHTPMYLFELS 62
QY 65 NLSFIDICSSSVTPPKMLBGLLEBKRTISFDNCITQLEFHLFACAEIFLLIIIVADRYV 124
DB 63 NLSFSDICFSSVTMPKLLQNMRSQDTSIPYGGCLAQTFPFMVGDMSFLLVMAVDRYV 122
QY 125 AICTPLHYPMVMNRVCIOVFLALMGCTVHSLGQFLTRIRLYCGPNIIDSYFCDPVLY 184
DB 123 AICFPLHYTISMPKCTCGLVLLMLTSHAMHTLALRLFCENNVVLANFCDLFLV 182
QY 185 IKACITDTYTLGLIYVNSGTTSLSCFLAVVTSYMLVLSLR-HSAGEKALSTCSAH 243
DB 183 LKACSDTYINELMIFMTSLTIIIPFLIYMSYARISILVPSYQGIKVFSTCSH 242
QY 244 FMVVALFEGPCIFITRRP--DTSFSIDKVVSVFYVTPPLNPFITLREBEVKSAM 298
DB 243 LSVVSLFYGITIGLYLCPAGANSTVKEMVAMMTVTPMLNPITSLRDKMRAL 299

RESULT 6
F23701
Olfactory receptor 17 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C:Accession: F23701
R/Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A>Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556; PMID:1840504
A:Accession: F23701
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-327 <BUC>
A:Cross-references: GB:M64386; NID:g205833; PIDN:AAA41749.1; PID:g205834
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 41.0%; Score 660; DB 2; Length 327;
Best Local Similarity 43.0%; Pred. No. 2e-49;
Matches 135; Conservative 61; Mismatches 98; Indels 20; Gaps 5;

QY 1 MDSLNT-RTTEVFVGLTDNRVLEMLPFMAFSAIYMLTSGNIIIIATVTPSLHTPM 59
DB 1 MERRNSGRVSEVLLGFAPAPARLVLLFPLSLXVLYVTEMLIIIRNRPHTLHKM 60
QY 60 YFPLNLSFIDICSSSVTPPKMLEGLLEBKRT-----ISFNCITQLEFHLFACAEIFLL 115
DB 61 YFPLNLSFIDICSSSVTPPKMLEGLLEBKRT-----ISFNCITQLEFHLFACAEIFLL 120
QY 116 IIVAYRYVATCTPLHYPMVMNRVCIOVFLALMGCTVHSLGQFLTRIRLYCGPNIID 175
DB 121 AVWAYRYVATCTPLHYPMVMNRVCIOVFLALMGCTVHSLGQFLTRIRLYCGPNIID 180
QY 176 SYCDVPLVTKLACTD-----TYLTGLIYVNSGTTSLSCFLAVVTSYMLVLSLRH 228

DB 181 HPCDVSPLNLSCTDMSTAEITDVLAFILGLPSLVGASMAITGAM-----RTP 234
QY 229 SAEGROKALSTCSAHFMVVALFFGPCIPIYTRPD--TSFSIDKVVSVFYVTPPLNPI 286
DB 235 SAAGRHKASFTCSHLLTVIIFYAASIFYABPKALSDPTNKLVSUVAIVPLFNPII 294
QY 287 YTLRNEEVSAMKQ 300
DB 295 YCLRNDVRRALR 308

RESULT 7
A46247
Olfactory receptor OR3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C:Accession: A46247
R/Hef, P.; Hermans-Borgmeyer, I.; Attieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinemann
Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992
A>Title: Spatial pattern of receptor expression in the olfactory epithelium.
A:Reference number: A46247; MUID:93028384; PMID:1384038
A:Accession: A46247
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-312 <REF>
A:Cross-references: GB:M64005; NID:g200153; PIDN:AAA39862.1; PID:g200154
A>Note: Sequence extracted from NCBI backbone (NCBI:P.115362)
C:Superfamily: olfactory receptor OR14

Query Match 40.9%; Score 659.5; DB 2; Length 312;
Best Local Similarity 44.3%; Pred. No. 2.1e-49;
Matches 133; Conservative 58; Mismatches 92; Indels 17; Gaps 3;

QY 12 FVFLGLTDNRVLEMLPFMAFSAIYMLTSGNIIIIATVTPSLHTPMYFELSIFDI 71
DB 12 FLMGVSDBPHLEIIFFAVILASVLTIVGNLTIIILSHLDARLHTPMYFELSISLDL 71
QY 72 CHSSVTPPKMLEGLLEBKRTISFDNCITQLEFHLFACAEIFLLIIIVADRYVATCTPLH 131
DB 72 ARTTSVPPQMLNKLMPDITISYGCCTQIVFLPMLGATECTILVMAFDRYVAVCRPLH 131
QY 132 YNNVMNRVCIOVFLALMGCTVHSLGQFLTRIRLYCGPNIIDSYFCDPVPLVTKLACTD 191
DB 132 YNTVMNPRLCWGLAASIMWGLGNSVIGSTFTLQPLFCGRVRYNDPLCGVPMITKACGD 191
QY 192 TYLTGLIYVNSGTTSLSCFLAVVTSYMLVLS-----LRKASAEGRQALSTCSAH 243
DB 192 TSL-----NEAVLVNGVCTPFTVVPVSIVLSCYPIADAVMKIRSVBGRRAFTCVSH 244
QY 244 FMVVALFEGPCIFITRRP--DTSFSIDKVVSVFYVTPPLNPFITLREBEVKSAMKQ 301
DB 245 LVVVFPLFYSAIYGLILPKAKSSNOCGRFISLFSVTPVMPVNLITLNNKEVKGALGR 304

RESULT 8
H23701
Olfactory receptor 19 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C:Accession: H23701
R/Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A>Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556; PMID:1840504
A:Accession: H23701
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-314 <BUC>
A:Cross-references: GB:M64388; NID:g205837; PIDN:AAA41751.1; PID:g205838
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.9%; Score 658.5; DB 2; Length 314;

Best Local Similarity 42.8%; Pred. No. 2.6e-49;
Matches 130; Conservative 65; Mismatches 106; Indels 3; Gaps 2;

```
OY 1 MDLSNORVTEFVFLGLTDRNVLEMLFFMAFSATYMLTSGNLIITATVPTSLHTPMY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTRRNOATFOFLGPPPEYQHLFYALPLANYLTLLGNLIITLLDLSHTPMY 60
OY 61 FPLSNLSFIDICHSSVTPVKMLBGLLEKRTISFDNCITOLFPLHFAEAFILLIIVAY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LPLSNLSFADLCSSVTPMKLQNMQOVPSIPYAGCLAQYFFLFGDGLFLVAMAY 120
OY 121 DRYVAICTPLHYPNVMNRVCIOLVFALMLGTVHSLGQFPLTRLPYCGPNIIDSYFCD 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DRYVAICFPLHYMSIMPKLCSLVIVLSWVLTTFHAMLHTLLMARLSFCEDSVIPHYFCD 180
OY 181 VPLVIKACDITYLTGLIYVNSGTISLSCFLAVVTSYMTVLVLRK-HSABGRQKALST 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 MSTLLKACSDTMDNEALIFLGGPIVLPPLLIIVSIVARISSIFVPSSQSTHKAFT 240
OY 240 CSAHFVVALFPGPCIFITRPTDSFSIDK--VVSVYTVVTPPLNPFITLRNEEYKSA 297
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 CGSLSTVSLFPGYVIGLVCPSANNSTVAKETWMSLMTVTPMLNPFISLRNRDKDA 300
OY 298 MKQL 301
    |||:
Db 301 LEKI 304
```

RESULT 9

Olfactory receptor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: S51356; S47014

R/Gat, U.; Nekrasova, E.; Lancel, D.; Nacochin, M.

A/Title: Olfactory receptor proteins. Expression, characterization and partial purification

A/Reference number: S51356; MUID:95045546; PMID:7957207

A/Accession: S51356

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-309 <GAT>

A/Cross-references: EMBL:X80671; NID:9517365; PIDN:CAAS6697.1; PID:9517366

R/Gat, U.; Nekrasova, E.; Lancel, D.; Nacochin, M.

A/Title: Olfactory receptor proteins. Expression, characterization and partial purification

A/Reference number: S47014

A/Accession: S47014

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-309 <GA2>

A/Cross-references: EMBL:X80671; NID:9517365; PIDN:CAAS6697.1; PID:9517366

C/Superfamily: olfactory receptor OR14

Query Match 40.8%; Score 657.5; DB 1; Length 309;
Best Local Similarity 44.3%; Pred. No. 3.1e-49;

Matches 136; Conservative 56; Mismatches 112; Indels 3; Gaps 2;

```
OY 1 MDLSNORVTEFVFLGLTDRNVLEMLFFMAFSATYMLTSGNLIITATVPTSLHTPMY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 MGTNHAADVAVFVGLTKPELLLPFFFLVIVYVTVGNLIMILLIIVSPLHTPMY 61
OY 61 FPLSNLSFIDICHSSVTPVKMLBGLLEKRTISFDNCITOLFPLHFAEAFILLIIVAY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 YFLSSLSFVDLCYSTVITPKLVNPLFGKKNFTTSECAQOFFFAIVVTEGYLLTWAY 121
OY 121 DRYVAICTPLHYPNVMNRVCIOLVFALMLGTVHSLGQFPLTRLPYCGPNIIDSYFCD 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 DRYVAICRPLHYVMSRISLLVLAFLGLFSAVVHTSAMNLSFCKSYIISHYFCD 181
OY 181 VPLVIKACDITYLTGLIYVNSGTISLSCFLAVVTSYMTVLVLRK-HSABGRQKALST 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 ALPLKLKACNTMLNELLIIFIGIANTLVPTLAVASIVPFCISILIRISSEGRSKAFGT 241
```

```
OY 240 CSAHFVVALFPGPCIFITRPTDSFSI--DKVSVYTVVTPPLNPFITLRNEEYKSA 297
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 242 CSSHLMAGVFPFSIFPWLKPKSSNSLGEKXSVYFTTVIPMLNPLIYSLRNKOVKA 301
OY 298 MKQLROR 304
    |||:
Db 302 LGRFSVR 308
```

RESULT 10

Olfactory receptor - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999

C/Accession: S20572

R/Parmentier, M.; Libert, F.; Schumann, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;

Nature 355, 453-455, 1992

A/Title: Expression of members of the putative olfactory receptor gene family in mammali

A/Reference number: S20571; MUID:92131132; PMID:1370859

A/Accession: S20572

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-314 <PAR>

A/Cross-references: EMBL:X64994; NID:932085; PIDN:CAA46127.1; PID:932086

C/Superfamily: olfactory receptor OR14

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.7%; Score 656; DB 2; Length 314;
Best Local Similarity 43.4%; Pred. No. 4.2e-49;

Matches 134; Conservative 67; Mismatches 104; Indels 4; Gaps 3;

```
OY 5 NOTRVTEFVFLGLTDRNVLEMLFFMAFSATYMLTSGNLIITATVPTSLHTPMYFPLS 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 NOTRISDFLLGLPIPEQONLCYALFLMYLTLLGNLIITLLDLSHTPMYFLFS 64
OY 65 NLSFIDICHSSVTPVKMLBGLLEKRTISFDNCITOLFPLHFAEAFILLIIVAYDRYV 124
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 NLSFSDLCFSSVITPKLQNMQNDPSIPADCLTMVFFLLFGDLESFLLVMAADRYV 124
OY 125 ALCTPLHYPNVMNRVCIOLVFALMLGTVHSLGQFPLTRLPYCGPNIIDSYFCDVPTV 184
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 ALCPPLHYTALMSPMCLALVALSWLTFHAMLHTLLMARLFCADNVPHFCDMSAL 184
OY 185 IKLACTDYLTGLIYVNSGTISLSCFLAVVTSYMTVLVLRK-HSABGRQKALSTCSAH 243
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 LKLAEPDTRNEMVITIMGLIIVIPFLLISYAIIVSILKVPSSKIGKAFSTCGSH 244
OY 244 FMVVALFPGPCIFIT--TRPDTSFSIDKVVSVFYTVTPPLNPFITLRNEEYKSAHQ- 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 LSVVSLFYGTVIGLVCSSANSSTLKDTWAMMYTVVTPMLNPFISLRNRDKGALSrv 304
OY 301 LRQOVFFFT 309
    |||:
Db 305 IHQKTFPS 313
```

RESULT 11

Olfactory receptor 115 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999

C/Accession: A37286

R/Buck, L.; Axel, R.

Cell 65, 175-187, 1991

A/Title: A novel multigene family may encode odorant receptors: a molecular basis for ol

A/Reference number: A23701; MUID:91191556; PMID:1840504

A/Accession: A37286

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-314 <BUC>

A/Cross-references: GB:64392; NID:9205845; PIDN:AAA1755.1; PID:9205846

C/Superfamily: olfactory receptor OR14

C; Keywords: G protein-coupled receptor; transmembrane protein.

Query Match	40.7%	Score 656;	DB 2;	Length 314;
Best Local Similarity	41.7%;	Pred. No. 4.2e-49;		
Matches 130;	Conservative 71;	Mismatches 107;	Indels 4;	Gaps 3;

```

QY      1  MDSLNGQTEEVFLGFLDNRVLBMLFPMASAIYMLLSGNILIIITVTPPSLHTEPMY  60
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1  MTERNGVYISQFLFLFLPPIPSRHQNVFALFISMILTVLGNILIIITLHDSHATPMY  60
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61  FFLSNLSFIDICHSSTVVPKMLEGLLEKRTISFNCITQJEFLLFPAQAFILLIAY  120
      61  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61  LFLSTLSFSDLCFSSVTPMKLLQNNQSOVPSIPFAGCITQJFYFYFLPDLSEFLVAMAY  120
      61  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      121  DRYAVALCPFLHPYNNMRVCIOLVFALMLGTVSLGQTYLTRLPYCGRNIIIDSYCD  180
      121  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121  DRYAVALCPFLHPYMSPKLCVSLVLSWLTTFHAMLHTTILMARLSFCADMMIPHEPCD  180
      121  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      181  VPLVYKALCTDYLTGLIIVTNSGTISLSCFLAANTSYMVLVSLRK-HSABGRKALST  239
      181  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      181  ISPLLKSLCSQTHNVELVIFVMGGIYIYIPEVLIIVSARVAASILKPSVGRGIKIPST  240
      181  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      240  CSAHPMVVALPFGPCIFRYTRPDTSIDK-VVSVFTVTVPLINPFIYTLRNEVUSA  297
      240  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      241  CGSHLSVLSLGYGTIIIGLYCLPSANNSTYVKETVAMAMTYVTPEMLNPIYSLRNDMKEA  300
      241  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      298  M-KQLRRQVFP 308
      298  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      301  LIRVLCKKKITF 312
      301  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 12
S20571
olfactory receptor - dog
C:/Species: Canis lupus familiaris (dog)
C:/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 26-Aug-1999
C:/Accession: S20571
R:/ParentIdentifier, M.; Liberty, F.; Schumans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;
Nature 355, 453-455, 1992
A:/Title: Expression of members of the putative olfactory receptor gene family in mammalian
A:/Reference number: S20571; MUID:92131132; PMID:1370859
A:/Accession: S20571
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-113 <PAR>
A:/Cross-references: EMBL:X64996; NID:9890; PIDD:CAA6129.1; PID:9891
C:/Superfamily: olfactory receptor OR14
C:/Keywords: G protein-coupled receptor; transmembrane protein

Query Match	40.7%;	Score 655;	DB 2;	Length 313;
Best Local Similarity	44.1%;	Pred. No. 5.1e-49;		
Matches 134;	Conservative 61;	Mismatches 105;	Indels 4;	Gaps 3;

[illegible]

QY	298 MKOL 301
	:::::
Db	300 LRRV 303

```

RESULT 13
123701
Olfactory receptor 114 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C:Accession: 123701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for o
A:Reference number: A23701, MUID:91191556; PMID:1840504
A:Accession: 123701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-312 <BUC>
C:Cross-references: GB:M64391; NID:g205843; PIDN:AAA41754.1; PID:g205844
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match	40.6%;	Score 653.5;	DB 2;	Length 312;
Best Local Similarity	43.5%;	Pred. No. 6.9e-49;		
Matches 131;	Conservative 55;	Mismatches 112;	Indels 3;	Gaps 2;

OY	1	MDSLNQRTVEFVFLGILGDNRLBEMLFPMASAIYMLTLLSGVILIIIAVFPFSLHTPMY	60
		: : : : : : : : : : : : : :	
Db	1	MTGNNGTILIFLLILGLPIPSERHLLFALFLAMLTIIILGMLIIIVLRDLSHLMMPY	60
OY	61	FFLSNLSPIDICHSSVAVPKMLEGLLEBKRTISFDCNTTOLFFLHLFACABIFLLIIVAY	120
		: : : : : : : : : : : : : :	
Db	61	LFSLNLSFSDCLFSSVTPMKLIONNOSQVPSISYGCULTOLFEPFVFCGMESEFLVVMAY	120
OY	121	DRYVAICPELHYPNVMNRVCILQVFAMLGTSVLSQCTFLTIRLPYCGPIIIOISFCD	180
		: : : : : : : : : : : : : :	
Db	121	DRYVAICPELHYTITMSYKFCASLVLLMLLMTLHTLHTLIALLSPCKNVIILHFFCD	180
OY	181	VPLVYKACATDVTYLTGLIIVTNSGTISLSCPLAVVTSYMWILVLSRKH-SAEGRQALST	239
		: : : : : : : : : : : : : :	
Db	181	ISALLKIKSCSDIYVNEMLIYILGGIILIIIPFLIIVMSYVRIFPSSIKFPSIDIDYVFST	240
OY	240	CSAHFMVVALPEFGPCIFLYTRPDTSFSLDK--VVSVFVTVTYPLNPFYLYLRNBEVSA	297
		: : : : : : : : : : : : : :	
Db	241	CGSHLSVVTLYFGTIFGLYICLPSGNNISYVKELAMMMATVVTPLNPFYISLRNRMKSA	300
OY	298	M 298	
Db	301	L 301	

```

RESULT 14
S29711
olfactory factor OR37 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C:Accession: S29711
R:Raming, K.; Krieger, J.; Stroetmann, J.; Boehnoff, I.; Kubick, S.; Baumstark, C.; Bressan, R.;
Nature 361, 353-356, 1993
A:Title: Cloning and expression of odorant receptors.
A:Reference number: S29707; MUID:93149273; PMID:7678922
A:Accession: S29711
A:Molecule type: mRNA
A:Residues: 1-305 <RAM>
A:Superfamily: olfactory receptor OR14

```

Query Match	40.0%	Score 645;	DB 2;	Length 305;
Best Local Similarity	42.1%	Pred. No. 3.6e-48;		
Matches 128;	Conservative	68;	Indels 10;	Gaps 3
13 VFGLDTRNRVLEMFPMAFSAIYMLTSGNLIITATVFTSLHTPMVFPSNLSFDIC 72				

Db 1 LLLGLSGYPTKEILLVYPIVLMVLIHTGNGVLLIASIPDSHLATPMYFPLGMLSPFLDIC 60
Qy 73 HSSVTVKMLLEGLLEKRTISFQNCITQLPFLHLFACAEIFLLITVAYDRYVAICTPLHY 132
Db 61 YTTSSVSTVSLSKGRNIFSQCCTQVMVGFPMGSTECLLGMAFPDRIYALCNPLRY 120
Qy 133 PNVNMRVCIQLVFALMLGQTVHSLGQFTLIRLPYCGPNIIDSYFCDVPLVIKLAQDTF 192
Db 121 SVINSEKVVYMASASWFGGINSVQTSIAMRLPFCGNVYINHFCEVLAVLKACADI 180
Qy 193 YLNGILLVNTSGTISLSCFLAVTSTVNVILVS-LRKSASGRKALSTCSAHPNVVALLFF 251
Db 181 SLNIVTWISNMAFLVPLLLIFPSYVLLITLIRMSASGRRRASFSTCSAHLTVVIFY 240
Qy 252 GPCTFIYTRP-----DTSFSIDKVVSVFYVTVPLNPFITYTLRNEEYKSAHQ-LR 302
Db 241 GTIFSMYAKRSQDLTGKDFQTSBKISLIFYGVTPMLNPIIYSLRNKDYKAAVKYIK 300
Qy 303 QROV 306
Db 301 QXYI 304

RESULT 15

JC5200
Chemoreceptor TB334 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
C:Accession: JC5200, PC4302
R:Thomas, M.B.; Haines, S.L.; Akesson, R.A.
Gene 178, 1-5, 1996
A:Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
A:Reference number: JC5200; MUID:97080538; PMID:8921883
A:Accession: JC5200
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-311 <TH01>
A:Cross-references: GB:U50947; NID:g1256388; PIDN:AAC52909.1; PID:g1256389
A:Accession: PC4302
A>Status: preliminary
A:Molecule type: protein
A:Residues: 146-153;265-272 <TH02>
A:Experimental source: taste bud
C:Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C:Genetics:
A:Gene: tb334
C:Superfamily: olfactory receptor OR14
C:Keywords: olfaction; taste bud; transmembrane protein
F:24-47/Domain: transmembrane #status predicted <TM1>
F:56-77/Domain: transmembrane #status predicted <TM2>
F:99-118/Domain: transmembrane #status predicted <TM3>
F:138-162/Domain: transmembrane #status predicted <TM4>
F:195-217/Domain: transmembrane #status predicted <TM5>
F:236-258/Domain: transmembrane #status predicted <TM6>
F:271-291/Domain: transmembrane #status predicted <TM7>

Query Match 40.0%; Score 644.5; DB 2; Length 311;
Best Local Similarity 42.3%; Pred. No. 4,1e-48;
Matches 127; Conservative 65; Mismatches 105; Indels 3; Gaps 2;

Qy 5 NQRTVTEFVPLGLTDNRVLEMLFPMASAIYMLTSGNIIIIATVFTPSLHTPMYFELS 64
Db 3 NQSSVSEFFLRGISGPEQQLLYGLFLCMVLTVLGNVLIILAIIGSDPHLHTPMYFELA 62
Qy 65 NLSFIDICHSVVTPKMLLEKRTISFQNCITQLPFLHLFACAEIFLLITVAYDRYV 124
Db 63 NLSPADMGILISYTKMLFNVQTCHTISYGLCTQMYLFFMFGDLDSFLAVWAYDRYV 122
Qy 125 AICPLIHPVNNMRVCIQLVFALMLGQTVHSLGQFTLIRLPYCGPNIIDSYFCDVPLV 184
Db 123 AICPLIHPVNNMRVCIQLVFALMLGQTVHSLGQFTLIRLPYCGPNIIDSYFCDVPLV 182
Qy 185 IKLACTDTYLTGLIIVNTSGTISLSCFLAVTSTVNVILVS-LRKSASGRKALSTCSAH 243

Db 183 MKLSCSDTHVNEELVLSGFGQTVLMVPEVSIIVSYHIVFAVLRIQSSGSSKAFSTCSSH 242
Qy 244 FMVVALFPGCTFIYTRPPTSPSIDKV--SVFYTVTPPLNPFITYTLRNEEYKSAHQ-LR 301
Db 243 LCVCVCFYGTLSVYLPSSVETTEKOVAAAMNTVTPMLNPFITYSLRNKDIKGLKRL 302

Search completed: August 12, 2003, 16:09:46
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:06:51 ; Search time 24 Seconds

(without alignments)
1660.142 Million cell updates/sec

Title: US-09-807-132-4

Perfect score: 1611
Sequence: 1 MDSLNQRTYTERFVFLGLTDN.....VKSAMKQLRQVFFTKSYT 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 479057 seqs, 127295195 residues

Total number of hits satisfying chosen parameters: 479057

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppa/PC7_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/prodata/1/pubppa/PC7US_PUBCOMB.pep:*
- 7: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/prodata/1/pubppa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/prodata/1/pubppa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/1/pubppa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/prodata/1/pubppa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/prodata/1/pubppa/US10C_NEW_PUB.pep:*
- 17: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the chance being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1611	100.0	313	12	US-10-017-161-426
2	1611	100.0	313	15	US-10-020-382-7
3	1380	85.7	308	11	US-09-832-522-82
4	1377	85.5	305	9	US-09-761-288-86
5	1377	85.5	305	11	US-09-898-586-86
6	1271	78.9	280	10	US-09-800-321A-54
7	938	58.2	311	10	US-09-886-055-309
8	938	58.2	311	11	US-09-804-291-309
9	929	57.7	314	10	US-09-886-055-403
10	929	57.7	314	11	US-09-804-291-403
11	929	57.7	314	12	US-10-017-161-402
12	927.5	57.6	310	10	US-09-886-055-447
13	927.5	57.6	310	11	US-09-804-291-447
14	919	57.0	324	15	US-10-023-601-34
15	919	57.0	348	10	US-09-886-055-409

16	919	57.0	348	11	US-09-804-291-409	Sequence 409, App
17	919	57.0	348	12	US-10-017-161-396	Sequence 396, App
18	905	56.2	325	10	US-09-886-055-405	Sequence 405, App
19	905	56.2	325	11	US-09-804-291-405	Sequence 405, App
20	900	55.9	305	9	US-09-761-288-85	Sequence 85, App
21	900	55.9	305	11	US-09-898-586-85	Sequence 85, App
22	900	55.9	318	9	US-09-761-288-20	Sequence 20, App
23	900	55.9	318	10	US-09-886-055-79	Sequence 79, App
24	900	55.9	318	11	US-09-898-586-20	Sequence 79, App
25	900	55.9	318	11	US-09-804-291-79	Sequence 21, App
26	900	55.9	318	15	US-10-020-382-21	Sequence 52, App
27	893	55.4	302	11	US-09-800-321A-52	Sequence 398, App
28	893	55.4	302	12	US-10-017-161-398	Sequence 237, App
29	889	55.2	308	10	US-09-886-055-237	Sequence 237, App
30	889	55.2	308	11	US-09-804-291-237	Sequence 239, App
31	889	55.2	308	12	US-10-017-161-414	Sequence 414, App
32	888	55.1	311	10	US-09-886-055-401	Sequence 401, App
33	888	55.1	311	11	US-09-804-291-401	Sequence 390, App
34	888	55.1	311	12	US-10-017-161-390	Sequence 239, App
35	878	54.5	343	10	US-09-886-055-239	Sequence 239, App
36	878	54.5	343	11	US-09-804-291-239	Sequence 416, App
37	878	54.5	343	12	US-10-017-161-416	Sequence 416, App
38	871	54.1	234	10	US-09-746-284-4	Sequence 51, App
39	869	53.9	308	11	US-09-800-321A-51	Sequence 268, App
40	869	53.9	310	12	US-10-017-161-268	Sequence 25, App
41	866	53.8	286	11	US-09-800-321A-25	Sequence 407, App
42	866	53.8	313	10	US-09-886-055-407	Sequence 407, App
43	865	53.7	292	12	US-09-804-291-407	Sequence 504, App
44	865	53.7	292	12	US-10-017-161-504	Sequence 406, App
45	865	53.7	307	12	US-10-017-161-406	

ALIGNMENTS

RESULT 1
US-10-017-161-426
; Sequence 426, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 08435/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 426
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-426

Query Match	Score	DB 12	Length	313
Best Local Similarity	100.0%	Pred. No. 2.1e-148		
Matches 313; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDSLNQRTYTERFVFLGLTDNRYLEMFFMFAFAIYMLTSGNLIILIAITVFPSPHTPMY	60	
DB	1	MDSLNQRTYTERFVFLGLTDNRYLEMFFMFAFAIYMLTSGNLIILIAITVFPSPHTPMY	60	
QY	61	FFLSNLSFIDICHSVYVKMLGGLLBKRTISFNCITQFPFLHFAACABIFLLIIVAY	120	
DB	61	FFLSNLSFIDICHSVYVKMLGGLLBKRTISFNCITQFPFLHFAACABIFLLIIVAY	120	
QY	121	DRYVAICTPLHYPNMNMKVCITQVPAIMLGSTVSLGOTFTITLPGYCGNIIIDSYFCD	180	
DB	121	DRYVAICTPLHYPNMNMKVCITQVPAIMLGSTVSLGOTFTITLPGYCGNIIIDSYFCD	180	

QY 181 VPLVIKLACTDVTYLTGILIVNSGTISLSCFLAVVTSYMWILVSLRHSABGRQKALSTC 240
DB 181 VPLVIKLACTDVTYLTGILIVNSGTISLSCFLAVVTSYMWILVSLRHSABGRQKALSTC 240
QY 241 SAHFMVVALPFGPCIFITYRPTDSFSDIKVSVFYTVVTPPLNPFITYTLNNEEYKSAHQ 300
DB 241 SAHFMVVALPFGPCIFITYRPTDSFSDIKVSVFYTVVTPPLNPFITYTLNNEEYKSAHQ 300
QY 301 LRQROVFFTKSYT 313
DB 301 LRQROVFFTKSYT 313

RESULT 2

US-10-220-382-7
Sequence 7, Application US/10220382
Publication No. US2003011911A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandira
APPLICANT: YAO, Monique G.
APPLICANT: SMITH, Leo L.
APPLICANT: TRIBOUTLEY, Catherine
APPLICANT: LU, Dyung Alma M.
APPLICANT: YUE, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junming
APPLICANT: HARLAND, Lee
APPLICANT: WALSH, Roderick T.
APPLICANT: LO, Terence P.
APPLICANT: BOKROSKY, Mark L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0044 PCT
CURRENT APPLICATION NUMBER: US/10/220,382
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US2003011911A1 3082743CD1
US-10-220-382-7

Query Match 100.0%; Score 1611; DB 15; Length 313;
Best Local Similarity 100.0%; Pred. No. 2, le-148;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSLNQRYVEFEVLGTDNRVLEMLPFMAFSAYMLTSGNILLIATVTPSLHTPMY 60
DB 1 MDSLNQRYVEFEVLGTDNRVLEMLPFMAFSAYMLTSGNILLIATVTPSLHTPMY 60
QY 61 FFLSNLSFIDICHSVTVPKMLEGLLEKRTISFDCNCTQLPFLHFACAEIFLLIIVAY 120
DB 61 FFLSNLSFIDICHSVTVPKMLEGLLEKRTISFDCNCTQLPFLHFACAEIFLLIIVAY 120
QY 121 DRYVAICTPLHYPNVMMNRVCIOVFPALMCGTVHSGQTFILTRLPCGNNIIDSFYCD 180
DB 121 DRYVAICTPLHYPNVMMNRVCIOVFPALMCGTVHSGQTFILTRLPCGNNIIDSFYCD 180
QY 181 VPLVIKLACTDVTYLTGILIVNSGTISLSCFLAVVTSYMWILVSLRHSABGRQKALSTC 240
DB 181 VPLVIKLACTDVTYLTGILIVNSGTISLSCFLAVVTSYMWILVSLRHSABGRQKALSTC 240

QY 241 SAHFMVVALPFGPCIFITYRPTDSFSDIKVSVFYTVVTPPLNPFITYTLNNEEYKSAHQ 300
DB 241 SAHFMVVALPFGPCIFITYRPTDSFSDIKVSVFYTVVTPPLNPFITYTLNNEEYKSAHQ 300
QY 301 LRQROVFFTKSYT 313
DB 301 LRQROVFFTKSYT 313

RESULT 3

US-09-832-522-82
Sequence 82, Application US/09832522
Publication No. US20030091563A1
GENERAL INFORMATION:
APPLICANT: Shenoy, Suresh G
APPLICANT: Gangolli, Raha A
APPLICANT: Rastelli, Luca
APPLICANT: Smitson, Glenda
APPLICANT: Padigar, Muralidhara
APPLICANT: Vernet, Corine
APPLICANT: Wolenc, Adam R
APPLICANT: Casman, Stacie J
APPLICANT: Tchernev, Velizar T
APPLICANT: Szekeres, Edward S
APPLICANT: Grose, William
APPLICANT: Alsobrook, John P
APPLICANT: Burgess, Catherine E
TITLE OF INVENTION: No. US20030091563A1 GPCR-Proteins and Nucleic Acids Encoding S.
FILE REFERENCE: 15966-767
CURRENT APPLICATION NUMBER: US/09/832,522
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/195,994
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/196,538
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/220,644
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/264,851
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: 60/199,964
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/268,567
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/199,955
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/259,641
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/200,176
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/199,948
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/199,956
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/218,995
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 82
LENGTH: 308
TYPE: PRT
ORGANISM: Mus musculus
US-09-832-522-82

Query Match 85.7%; Score 1380; DB 11; Length 308;
Best Local Similarity 85.6%; Pred. No. 5, le-126;
Matches 262; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDSLNQRYVEFEVLGTDNRVLEMLPFMAFSAYMLTSGNILLIATVTPSLHTPMY 60
DB 1 MDSLNQRYVEFEVLGTDNRVLEMLPFMAFSAYMLTSGNILLIATVTPSLHTPMY 60
QY 61 FFLSNLSFIDICHSVTVPKMLEGLLEKRTISFDCNCTQLPFLHFACAEIFLLIIVAY 120
DB 61 FFLSNLSFIDICHSVTVPKMLEGLLEKRTISFDCNCTQLPFLHFACAEIFLLIIVAY 120

Db 61 FFLSNLSFIDICHSSTVTPKMLFGLLBERKTSFDFNCIAQLFPLHAFACSEIFLITIMAY 120
QY 121 DRVVAICTPLHYNNWMMKVCQVLVFLMLGTTIHSVGTFTLIRLPGCPNIIDSFYCD 180
Db 121 DRVVAICTPLHYNNWMMKVCQVLVFLMLGTTIHSVGTFTLIRLPGCPNIIDSFYCD 180
QY 181 VPLVIACTDITYLTGILIVTNSGTTSLSCFLAVVTSYVWILVSLRKSABGRKALSTC 240
Db 181 VPLVIACTDITYLTGILIVTNSGTTSLSCFLAVVTSYVWILVSLRKSABGRKALSTC 240
QY 241 SAHFMMVTLFFGFCIFLYTRPDSSFSIDKVVSVFYVTVPLNPLIYTLNNEEVKTAMKH 300
Db 241 SAHFMMVTLFFGFCIFLYTRPDSSFSIDKVVSVFYVTVPLNPLIYTLNNEEVKTAMKH 300
QY 301 LROROV 306
Db 301 LRORRI 306

RESULT 4

US-09-761-288-86
; Sequence 86, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupler, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberky
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 86
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-288-86

Query Match 85.5%; Score 1377; DB 9; Length 305;
Best Local Similarity 85.9%; Pred. No. 1.1e-125;
Matches 262; Conservative 19; Mismatches 24; Indels 0; Gaps 0;
QY 1 MDSLNQTRVTEFVGLTDRNRLVLEMLFMAFSAIYMLTSGNILLITIAVTFPSLTPMY 60
Db 1 MDSLNQTRVTEFVGLTDRNRLVLEMLFMAFSAIYMLTSGNILLITIAVTFPSLTPMY 60
QY 61 FFLSNLSFIDICHSSTVTPKMLFGLLBERKTSFDFNCIAQLFPLHAFACSEIFLITIMAY 120
Db 61 FFLSNLSFIDICHSSTVTPKMLFGLLBERKTSFDFNCIAQLFPLHAFACSEIFLITIMAY 120
QY 121 DRVVAICTPLHYNNWMMKVCQVLVFLMLGTTIHSVGTFTLIRLPGCPNIIDSFYCD 180
Db 121 DRVVAICTPLHYNNWMMKVCQVLVFLMLGTTIHSVGTFTLIRLPGCPNIIDSFYCD 180

Db 121 DRVVAICTPLHYNNWMMKVCQVLVFLMLGTTIHSVGTFTLIRLPGCPNIIDSFYCD 180
QY 181 VPLVIACTDITYLTGILIVTNSGTTSLSCFLAVVTSYVWILVSLRKSABGRKALSTC 240
Db 181 VPLVIACTDITYLTGILIVTNSGTTSLSCFLAVVTSYVWILVSLRKSABGRKALSTC 240
QY 241 SAHFMMVTLFFGFCIFLYTRPDSSFSIDKVVSVFYVTVPLNPLIYTLNNEEVKTAMKH 300
Db 241 SAHFMMVTLFFGFCIFLYTRPDSSFSIDKVVSVFYVTVPLNPLIYTLNNEEVKTAMKH 300
QY 301 LRORQ 305
Db 301 LRORR 305

RESULT 5

US-09-898-586-86
; Sequence 86, Application US/09898586
; Publication No. US20030077794A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: No. US20030077794A1el Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-638CIP
; CURRENT APPLICATION NUMBER: US/09/898,586
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 09/761,288
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 86
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-586-86

Query Match 85.5%; Score 1377; DB 11; Length 305;
Best Local Similarity 85.9%; Pred. No. 1.1e-125;
Matches 262; Conservative 19; Mismatches 24; Indels 0; Gaps 0;
QY 1 MDSLNQTRVTEFVGLTDRNRLVLEMLFMAFSAIYMLTSGNILLITIAVTFPSLTPMY 60
Db 1 MDSLNQTRVTEFVGLTDRNRLVLEMLFMAFSAIYMLTSGNILLITIAVTFPSLTPMY 60
QY 61 FFLSNLSFIDICHSSTVTPKMLFGLLBERKTSFDFNCIAQLFPLHAFACSEIFLITIMAY 120
Db 61 FFLSNLSFIDICHSSTVTPKMLFGLLBERKTSFDFNCIAQLFPLHAFACSEIFLITIMAY 120
QY 121 DRVVAICTPLHYNNWMMKVCQVLVFLMLGTTIHSVGTFTLIRLPGCPNIIDSFYCD 180
Db 121 DRVVAICTPLHYNNWMMKVCQVLVFLMLGTTIHSVGTFTLIRLPGCPNIIDSFYCD 180
QY 181 VPLVIACTDITYLTGILIVTNSGTTSLSCFLAVVTSYVWILVSLRKSABGRKALSTC 240
Db 181 VPLVIACTDITYLTGILIVTNSGTTSLSCFLAVVTSYVWILVSLRKSABGRKALSTC 240

Qy	241	SAHEVVALERPGPCFPIYTRDTSFSIDKVVSVFYVVTPLNLPFIYTLRNEVKSAMKQ	300
		: : : : : : : : : :	
Db	241	SAHEVVALTFPGPCFLYTRDSSFSIDKVVSVFYVVTPLNLPFIYTLRNEVKSAMKH	300

QY	301	LRQRQ	305
		:	
Db	301	LRQRR	305

RESULT 6
US-09-800-321A-54

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; Sequence 54, Application US/09800321A
; Publication No. US20030068671A1
; GENERAL INFORMATION:

Query Match	78.9%	Score 1271	DB 11	Length 280
Best Local Similarity	86.1%	Pred. No. 1.9e-115		
Matches 241	Conservative 17	Mismatches 22	Indels 0	Gaps 0

QY 61 FFLSNLSFIDICHSVTPVKMLBGLLERRKTSFNDNCITQLFELHALFACAEIPLLIYAY 120
Db 61 FFLSNLSFIDICHSVTPVKMLBGLLERRKTSFNDNCITQLFELHALFACAEIPLLIYAY 120

QY 12 DRVALCTGLHYPNWMMNRVCGLVEFALMDGTHSVGGQFLTRLYCYGPNIIIDSYFC 180

Db 121 DRVALCTGLHNSNMWNRVCQGLVEFALMDGTHSLVQFLTRLYCYGPNIIIDSYFC 180

QY 181 VPLVLTACTDPTYLGLILVINSGTLSLCPAAVTSYMTLVLSLRGHSABGQKALSTC 240

Db 181 VPLVLTACTDPTYLGLILVINSGTLSLCPAAVTSYTLVLSLRGHSABGQKALSTC 240

QY 241 SAHFMVVALFFGPCIPIYTRPDTSFSIDKVSVFYTVTP 280
|||:|||||
Db 241 SAHFMVTLFFGPCIPIYTRPDSFSIDKVSVFYTVTP 280

RESULT 7
US-09-886-055-309

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;
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
;

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! APPLICANT: ZOZULYA, SERGEY
! TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
! TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS

Query Match	58.2%;	Score 938;	DB 10;	Length 311;
Best Local Similarity	55.4%;	Pred. No. 4.5e-83;		
Matches 170; Conservative	59;	Mismatches 76;	Indels 2;	Gaps 1

Qy 1 MDSLNQTRVTEFVFGLGTDRKVLNMLEMFPMASAIWMLTSSGILIIATVFPSPSLHTPMY 60
| : | |||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 MEKIN--NTVEFIFMGLSQSPEIEKKCFVPVSFFYYIILLGNLLIMLTVCLSNLPKSPMY 58

Qy 61 PFLSNISFDICHSSVTVPKMLEGILLERKTISPNCITQLFPLHLPACAEIFLLITAY 120
|||:::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 59 PFLSLFSVNDICYSSTAPAKMIVDLAKDKTISYVGCMQLGLGVHFEGCTEIFILTWAY 118

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Qy      121 DRYAICTPLHYPNVMMNRVCIQLVAFALMGSTVHSLGQETLTIRLPCGPNIIIDSYFCD 180
      ||||| |||| :: ||| ::| ::| ::| ::| ::|
Db      119 DRYAICKPLHYMTIMNRCTCNKMLGTWGGFSLHIIQVALVQOLPFCGPNIEDHLYFCD 178
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[illegible]

QY 241 SAHFWVALFEGPCTFIITYRBDTSSIDKVVSVFYVTVPLINPFITLRNEEVKSANKQ 300
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Db 239 GSHIMAVVFEGPCTFEMRYBDDTTSEEDKKVAVFYIITPMINPLIYTLRNAEVRNANKK 298

QY	301	LRQRYF	307
DB	299	LMGRNF	305

Db 299 IMGRNVE 305

; APPLICANT: ZOZULIA, SERGEY
 ; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
 ; FILE REFERENCE: P 0278005


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; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 309
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-309

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Query Match      58.2%; Score 938; DB 11; Length 311;
Best Local Similarity 55.4%; Pred. No. 4.5e-83;
Matches 170; Conservative 59; Mismatches 76; Indels 2; Gaps 1;

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Qy 1 MDSLNQRTVEFEFLGIDTRVLEMLFMAFSAIYMLTSGNLIITATVFTSHTPMY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEXIN--NVEFTFWSQSPELEKVCVFVSEFFYIILINLLIMLTVCILNLEKSPMY 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 FPLSNLSFIDICSHSVTPMTEGLLEKRTISFDCITQLPFLHFAACAFILLIIVAY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 FPLSPISFVDICSVSVAPRMIVDLAKDITISVGMQLQGVHFGCEIFILTYMAY 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 DRVVAICTPLHYNNMNMVCIQVFLMLTGVVHSLGQFTLRLPYCGPNIIDSPCD 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 DRVVAICKPLHYNTIMRERCNKLQGTWVGFLHSIIQVALVVOQFCGPNEDHYFCD 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 VPLVIACTDLYLTGILIVTNSGTLSLSCFLAVTSYMWILVSLRHSAGROKALSTC 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 VHVVLKLAETTYIVGVVANSSTIALSGFVILLISLILVSLRQSABGRKALSTC 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 SAHEMVVALPFGPCIFITRPTDSFSDIKVSVFYTVTPPLNPFITTLNBEVKSKAMQ 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 239 GSHIAMVVFPGCFITVYMPKPDFTFSEDKNVAVFYITITPLNPLIYTLNNAEVKNAKMK 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 LROROWP 307
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 LMGRAWP 305
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 9
US-09-886-055-403
; Sequence 403, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SUBSTANCES
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 403
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-055-403

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Query Match      57.7%; Score 929; DB 10; Length 314;
Best Local Similarity 53.1%; Pred. No. 3.4e-82;
Matches 165; Conservative 67; Mismatches 79; Indels 0; Gaps 0;

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Qy 1 MDSLNQRTVEFEFLGIDTRVLEMLFMAFSAIYMLTSGNLIITATVFTSHTPMY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDVGNKSTSEFPLGLSNSEMLQMFVNFSLIYAVMGNSLIYIYVDPHLSPMY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 FPLSNLSFIDICSHSVTPMTEGLLEKRTISFDCITQLPFLHFAACAFILLIIVAY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FLTNIISIIMSLASPATPMIDVLTGKHTISFDCITQLPFLHFTGTETILLAMSP 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 DRVVAICTPLHYNNMNMVCIQVFLMLTGVVHSLGQFTLRLPYCGPNIIDSPCD 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DRVVAICKPLHYASVSPQCVALLVASMIGVHSMQVIFALTLPCGPEVDSFPCD 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 VPLVIACTDLYLTGILIVTNSGTLSLSCFLAVTSYMWILVSLRHSAGROKALSTC 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LPVVPQACVDITVGLFMISTGIIALSCFIVLPMSYIVLVTVGHSSRGSSKALSTC 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 SAHEMVVALPFGPCIFITRPTDSFSDIKVSVFYTVTPPLNPFITTLNBEVKSKAMQ 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TAFIVVPLPFGPCIFITVYMPKPDFTFSEDKNVAVFYITITPLNPLIYTLRNGEVKIAMRK 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 LROROWP 311
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 LKRRFLNPKA 311
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 10
US-09-804-291-403
; Sequence 403, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 403
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-403

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Query Match      57.7%; Score 929; DB 11; Length 314;
Best Local Similarity 53.1%; Pred. No. 3.4e-82;

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Query Match	57.6%	Score 927.5;	DB 11;	Length 310;
Best Local Similarity	55.0%	Pred. No. 4.7e-82;		
Matches 170; Conservative	60;	Mismatches 78;	Indels 1;	Gaps 1;

301 KLQNRRTF 309

PRIOR APPLICATION NUMBER: 60/299,327

US-10-023-601-34

Matches 171; Conservative 50; Mismatches 83; Indels 0; Gaps 0;

Db 301 LKSR 304

PRIOR APPLICATION NUMBER: 60/213,812

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2003, 16:05:31 ; Search time 30 Seconds

(without alignments)
441.443 Million cell updates/sec

Title: US-09-807-132-4

Perfect score: 1611
Sequence: 1 MSLNQTRTREVFVFLGTLTN.....VKSAMQLRQROVFTKSTY 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	674.5	41.9	333	US-08-988-876-6	Sequence 6, Appl
2	667.5	41.4	309	US-08-988-876-5	Sequence 5, Appl
3	656	40.7	314	US-08-988-876-7	Sequence 7, Appl
4	640	39.7	313	US-09-465-901-48	Sequence 48, Appl
5	639.5	39.7	321	US-08-748-506-18	Sequence 18, Appl
6	634.5	39.4	321	US-08-748-506-10	Sequence 10, Appl
7	628.5	39.0	321	US-08-748-506-20	Sequence 20, Appl
8	626.5	38.9	321	US-08-748-506-19	Sequence 19, Appl
9	623.5	38.7	321	US-08-748-506-11	Sequence 11, Appl
10	623.5	38.7	321	US-08-748-506-12	Sequence 12, Appl
11	617.5	38.3	321	US-08-748-506-13	Sequence 13, Appl
12	599.5	37.2	284	US-08-118-270-61	Sequence 61, Appl
13	599.5	37.2	284	PCT-US93-08528-61	Sequence 61, Appl
14	573	35.6	293	US-08-118-270-60	Sequence 60, Appl
15	573	35.6	293	PCT-US93-08528-60	Sequence 60, Appl
16	567	35.2	284	US-08-118-270-67	Sequence 67, Appl
17	567	35.2	284	PCT-US93-08528-67	Sequence 67, Appl
18	560.5	34.8	286	US-08-827-291A-2	Sequence 2, Appl
19	553.5	34.4	286	US-08-118-270-65	Sequence 65, Appl
20	553.5	34.4	286	PCT-US93-08528-65	Sequence 65, Appl
21	553.5	34.4	327	US-08-748-506-24	Sequence 24, Appl
22	551.5	34.2	327	US-08-748-506-14	Sequence 14, Appl
23	541	33.6	296	US-08-467-948A-2	Sequence 2, Appl
24	540.5	33.6	275	US-08-467-947A-2	Sequence 66, Appl
25	540.5	33.6	275	PCT-US93-08528-66	Sequence 66, Appl
26	540.5	33.6	275	US-08-118-270-66	Sequence 66, Appl
27	540.5	33.6	327	US-08-748-506-22	Sequence 22, Appl

28	540.5	33.6	327	US-08-748-506-23	Sequence 23, Appl
29	537	33.3	277	US-08-118-270-68	Sequence 68, Appl
30	537	33.3	277	PCT-US93-08528-68	Sequence 68, Appl
31	526.5	32.7	269	US-08-118-270-64	Sequence 64, Appl
32	526.5	32.7	269	PCT-US93-08528-64	Sequence 64, Appl
33	522.5	32.4	274	US-08-118-270-69	Sequence 69, Appl
34	522.5	32.4	274	PCT-US93-08528-69	Sequence 69, Appl
35	518.5	32.2	247	US-08-465-980-3	Sequence 3, Appl
36	518.5	32.2	247	US-09-053-303-3	Sequence 3, Appl
37	518.5	32.2	247	US-09-339-115-3	Sequence 3, Appl
38	518.5	32.2	247	PCT-US95-07093-3	Sequence 3, Appl
39	516.5	32.1	277	US-08-118-270-62	Sequence 62, Appl
40	516.5	32.1	277	PCT-US93-08528-62	Sequence 62, Appl
41	485.5	30.1	223	US-09-465-901-38	Sequence 38, Appl
42	475.5	29.5	273	US-08-118-270-63	Sequence 63, Appl
43	475.5	29.5	273	PCT-US93-08528-63	Sequence 63, Appl
44	473	29.4	222	US-09-465-901-44	Sequence 44, Appl
45	469.5	29.1	223	US-09-465-901-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-988-876-6
Sequence 6, Application US/08988876
Patent No. 6063526
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Vye, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 205814
US-08-988-876-6

```

Query March 41.9%; Score 674.5; DB 3; Length 333;
Best Local Similarity 43.9%; Pred. No. 1.5e-49;
Matches 133; Conservative 62; Mismatches 105; Indels 3; Gaps 2;

Qy 1 MDSINQTVTEFEVFGLTNDNRVLLELFFMAFSAIYMLTSGNILLIIVATFPPSIHTPMY 60
Db 1 MDSNRTRTFSEFLLGFPENNDDLOPLIYGLFLSMVLIVIVINISIIIVAILSDPCILTPMY 60
Qy 61 FFLSLNLSIDIDCHSSVTPPKMLEGLLEKRTISPDNCTOLPELHFPACAEIPLIIYAY 120
Db 61 FFLSLNLSFVDCIFISTVPPKMLVNIQTNNVITAGCTIOIFFLFVELDNPFLITIMAY 120
Qy 121 DRYAICPLHYPNVMNRVCIOLEFALMLGTVHSLGOTFLTRLPPCGNIIDSYECD 180
Db 121 DRYAICPLHYPNVITAMNYKLGFLVLVSIVISVHALQSLMLALPCTHLEIPIHYCE 180
Qy 181 VPLVIKLACTDVTYLGILIVTNSGTISLSCELAVTSYMWIVSL-RKHSAGRKALST 239
Db 181 PNOVIYQLTCSAPFLNDLIVITFTVLIVATVPLAGIRYSFKIVSSICAISSVHGKKARST 240
Qy 240 CSAHPMVVALP--GPCIFITRPDTPSSIDKVVSVFTVTVPLINPIYTLRNEEVKSA 297
Db 241 CASHLSVSLFPCYCTGLGAVLSSAANNSSQASATASVMYTVVTPMVNPFIVSLRNDVXSV 300
Qy 298 MKQ 300
Db 301 LKK 303

RESULT 2
US-08-988-876-5
; Sequence 5, Application US/08988876
; Patent No. 6063596
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988.876
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0441 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

```

      TOPOLOGY: linear
      IMMEDIATE SOURCE:
      LIBRARY: GenBank
      CLONE: J114667
      US-08-988-876-5

Query Match          41.4%; Score 667.5; DB 3; Length 309;
Best Local Similarity 41.8%; Pred. No. 5.4e-49;
Matches 130; Conservative 71; Mismatches 101; Indels 9; Gaps 3

Qy      1 MSLSNRTYEEVFVGLTIDNRVLEMLFEMAFSAIYMLTLGSLNIILIAATVFTPSLHTPMY 60
       1 MELENDTRIPEFLILGFSEBPTLOPFLRGLPLSMYLVTIIIGNLILLILAASDSHLHTPMY 60
Db
Qy      61 FFLSNISFDIDCHSSVTPKYLEGILLERKTISPDNCITQLFPLHLPACAEIFLLIIAY 120
       61 FFLANISFPDICFTCTTIIPKMLVMIQTRKVITYESCIIMYPFEELFAGIDNELLTVMAY 120
Db
Qy      121 DRVALCTPLAHYRNWNNRKVICLOLFALMLGTGHSGOTFELTRLPYCGPNIIIDSVPED 180
       121 DRMALCYPLAHWNINNPOLCSLLLYSWIMSALSHLLQTLMLRLSFCTHPQIPHPCF 180
Db
Qy      181 VPLVIKLACTDYVLTGILLIVNSGTTISLCPLAAVTSYMYLVLSLR-HSABGRORALST 239
       181 LNMIGILOASDFLNMMMLYPAALLGVAPLVGLVSYFKVISIRGISASHKYAKFSF 240
Db
Qy      240 CSAHFNVVALFFGPCIFIY--TRPDTSPSIDKVSVFYYVTPLPLNFYTLLNEEYKA 297
       241 CASHLSVSLFYCTSIGVYLSGAAPQSTHTSSVASVMYTVTPMLNPFYLSLNKDICKA 300
Qy      298 MKQLRROYEF 308
       :             |||
Db      301 L-----NWVF 305

RESULT 3
US-08-988-876-7
Sequence 7, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
Applicant: Lal, Preeti
Applicant: Bandman, Olga
Applicant: Hillman, Jennifer L.
Applicant: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
FAX: 650-845-4166

```

TELEX:
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 314 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 32086
 US-08-988-876-7

Query Match 40.7%; Score 656; DB 3; Length 314;
 Best Local Similarity 43.4%; Pred. No. 5.1e-46;
 Matches 134; Conservative 67; Mismatches 104; Indels 4; Gaps 3;

QY 5 NQRTVEVPLGLTDRNVLKEMLPFMAFSAIYMLTSGNLIITATVTPSLHTPMYFPLS 64
 DB 5 NQRTISDFLLGLPIQPEQONLCYALFLAMYLITLLGNLIITVLRHDSHTPMYFPLS 64
 QY 65 NLSFIDICHSVTPPKMLBGLLERKTIISFNCITQLFPLHFACAEFLIIIVAYDRYV 124
 DB 65 NLSFSDLCFSSVYIPFLQNMOMQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYV 124
 QY 125 AICTPLHYNNMMRVCIQVFLMTLGTGTVHSLGOTFLTRLPYCGPNIIDSFCVPLV 184
 DB 125 AICFPLHYNNMSPMLCLALVALSWLVTTFHAMLTLMAELCFQADNVIHPFFCDMSAL 184
 QY 185 IKLACTDYLTGILIVTNSGTISLSCFLAVTSSYVILVLSRK-HSAEGROKALSTCSAH 243
 DB 185 LKIAFSDTVNENVIPIFMGLIIVIPFLILISYAVISILKVPSSKIGCAFSICGSH 244
 QY 244 FMVVALFPGPCFIY--TRPDTSIDKVSVYTVTPPLNPFITTLRNEEYKAMKO- 300
 DB 245 LSVVSLFPGVIGLYLCCSSANSSITLKDVTVMAMVYTVTPMLNPFYISLRNRDKGALSRY 304
 QY 301 LRQROVFEPT 309
 DB 305 IHQKTFES 313

RESULT 4
 US-09-465-901-48
 Sequence 48, Application US/09465901
 Patent No. 6492143
 GENERAL INFORMATION:
 APPLICANT: Reed, Randall
 APPLICANT: Krautwurst, Dietmar
 TITLE OF INVENTION: Olfactory Receptor Expression Libraries
 FILE REFERENCE: 001107, 00105
 CURRENT APPLICATION NUMBER: US/09/465,901
 PRIOR FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: 60/112,605
 NUMBER OF SEQ ID NOS: 57
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 48
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Mus musculus
 FEATURE:
 OTHER INFORMATION: PCR primer
 US-09-465-901-48

Query Match 39.7%; Score 640; DB 4; Length 313;
 Best Local Similarity 44.9%; Pred. No. 1.1e-46;
 Matches 136; Conservative 51; Mismatches 106; Indels 10; Gaps 5;
 QY 5 NQRTVEVPLGLTDRNVLKEMLPFMAFSAIYMLTSGNLIITATVTPSLHTPMYFPLS 64
 DB 3 NQRTVEVPLGLTDRNVLKEMLPFMAFSAIYMLTSGNLIITATVTPSLHTPMYFPLS 62

QY 65 NLSFIDICHSVTPPKMLBGLLERKTIISFNCITQLFPLHFACAEFLIIIVAYDRYV 124
 DB 63 NFAMLEIWPFSYIPFPMILNIIITGHKTIISLACGFIQAFLYFGTTEPFLVAMSDRYV 122
 QY 125 AICTPLHYNNMMRVCIQVFLMTLGTGTVHSLGOTFLTRLPYCGPNIIDSFCVPLV 184
 DB 123 AICNPLRYATIMSKRVQVQVFCSSMWSGLLIIVPSSIVFOQPFQCPNIINHPFCDNPL 182
 QY 185 IKLACTDYLTGIL--IVTNSGTISLSCFLAV-VTSYVILVS-LRKHSAGROKALSTC 240
 DB 183 MELICADTSLVFLGVIAN---FSLGTLATATCTGILVTLIHPAKERKCAFSIC 239
 QY 241 SAHFMVVALFPGPCFIYTRPDTSS--FSIDKVSVYTVTPPLNPFITTLRNEEYKSA 297
 DB 240 SSHIIIVSLFPGSCIFMYVRSKNGQGBDHNRKVALNVTVPPLNPFITTLRNRKQKV 299
 QY 298 MKO 300
 DB 300 FRE 302

RESULT 5
 US-08-748-506-18
 Sequence 18, Application US/08748506
 Patent No. 6159707
 GENERAL INFORMATION:
 APPLICANT: Ronnelt et al.
 TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,506
 FILING DATE: 08-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,751
 FILING DATE: 09-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION: 74940
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5700
 TELEFAX: 312-616-5600
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-748-506-18

Query Match 39.7%; Score 639.5; DB 3; Length 321;
 Best Local Similarity 43.1%; Pred. No. 1.3e-46;
 Matches 132; Conservative 58; Mismatches 99; Indels 17; Gaps 4;
 QY 5 NQRTVEVPLGLTDRNVLKEMLPFMAFSAIYMLTSGNLIITATVTPSLHTPMYFPLS 64
 DB 11 NSLYKHAFAKFSVSPGECFLPLNLIIMFLVSLTGILVLAICTSPSLHTPMYFPLA 70
 QY 65 NLSFIDICHSVTPPKMLBGLLERKTIISFNCITQLFPLHFACAEFLIIIVAYDRYV 124

Db 71 NLSLEIGYTCVTPKMLQSLVSEAREISREGCATQMFPAFPGITECCLLAAMAFDRCM 130
Qy 125 AICTPLHYPMNMARVCIOVFLALMLGTVHSLGQTFILTRLPYCGPNIIDSFCVPLV 184
Db 131 AICSPHAYTRMSREVCALIAVSWMGCIIVSLGQTNFIFSLNFCGCEIDHFFCDLPPL 190
Qy 185 IKLACTDT-----YLTGILIVTNSGTTISLSCFLAVTSSVWVLVS-LRKSASGRQKA 236
Db 191 IALACGDTSQNEAIFVAVALCIS-----SPFLIIYSYVKILIAVLMPSGGRHKA 243
Qy 237 LSTCSAHFVVALFPGPCFIITYTRPDTSFS--IDKVSIVTYVTPLNPFITTLRNEEV 294
Db 244 LSTCSSHLVLTFLVFSACITLPRKSSHPGMDKFLALFTVVTSMNPDIYSLRNKEV 303
Qy 295 KSAMKO 300
Db 304 KAALRR 309

RESULT 6

US-08-748-506-10
Sequence 10, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnec et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: 74940
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-748-506-10

Query Match 39.4%; Score 634.5; DB 3; Length 321;
Best Local Similarity 42.8%; Pred. No. 3.4e-46;
Matches 131; Conservative 58; Mismatches 100; Indels 17; Gaps 4;

Qy 5 NQTRVTEFVLGLTDRNVLEMLFPMFSAIYMLTSGNIIIIATVFTPSLHTPMWFELS 64
Db 11 NLSIVKFAFAKSEVPGECFLFLNLLIMFLVSLTGNLTIVAICTSPSLHTPMWFELA 70
Qy 65 NLSFIDICSSVTPKMLBGLLERTKISFDNCTQLFPLHPACAEIFLLIIVAYDRYV 124
Db 71 NLSLEIGYTCVTPKMLQSLVSEAREISREGCATQMFPAFPGITECCLLAAMAFDRCM 130

Qy 125 AICTPLHYPMNMARVCIOVFLALMLGTVHSLGQTFILTRLPYCGPNIIDSFCVPLV 184
Db 131 AICSPHAYTRMSREVCALIAVSWMGCIIVSLGQTNFIFSLNFCGCEIDHFFCDLPPL 190
Qy 185 IKLACTDT-----YLTGILIVTNSGTTISLSCFLAVTSSVWVLVS-LRKSASGRQKA 236
Db 191 IALACGDTSQNEAIFVAVALCIS-----SPFLIIYSYVKILIAVLMPSGGRHKA 243
Qy 237 LSTCSAHFVVALFPGPCFIITYTRPDTSFS--IDKVSIVTYVTPLNPFITTLRNEEV 294
Db 244 LSTCSSHLVLTFLVFSACITLPRKSSHPGMDKFLALFTVVTSMNPDIYSLRNKEV 303
Qy 295 KSAMKO 300
Db 304 KAALRR 309

RESULT 7

US-08-748-506-20
Sequence 20, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnec et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: 74940
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-748-506-20

Query Match 39.0%; Score 628.5; DB 3; Length 321;
Best Local Similarity 43.5%; Pred. No. 1.1e-45;
Matches 130; Conservative 56; Mismatches 110; Indels 3; Gaps 2;

Qy 5 NQTRVTEFVLGLTDRNVLEMLFPMFSAIYMLTSGNIIIIATVFTPSLHTPMWFELS 64
Db 11 NLSIVKFAFAKSEVPGECFLFLNLLIMFLVSLTGNLTIVAICTSPSLHTPMWFELA 70
Qy 65 NLSFIDICSSVTPKMLBGLLERTKISFDNCTQLFPLHPACAEIFLLIIVAYDRYV 124
Db 71 NLSLEIGYTCVTPKMLQSLVSEAREISREGCATQMFPAFPGITECCLLAAMAFDRYV 130
Qy 125 AICTPLHYPMNMARVCIOVFLALMLGTVHSLGQTFILTRLPYCGPNIIDSFCVPLV 184
Db 131 AICSPHAYTRMSREVCALIAVSWMGCIIVSLGQTNFIFSLNFCGCEIDHFFCDLPPL 190

Qy 295 KSAMKQ 300
Db 304 KAALRR 309

RESULT 10
US-08-748-506-12
; Sequence 12, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-748-506-12

Query Match 38.7%; Score 623.5; DB 3; Length 321;
Best Local Similarity 43.1%; Pred. No. 2.9e-45;
Matches 129; Conservative 56; Mismatches 111; Indels 3; Gaps 2;
Qy 5 NOTRTEFVFLGLDNRVLEMLPFMAFSAIYMLTSGNIIIIITVFTPSLHTPMYFELS 64
Db 11 NSLSVKRFAPAKSEVGECEFLFTLLILMFVSLTGNLIALAICTSPSLHTPMYFELA 70
Qy 65 NLSFDICHSSVTPPKMLEGLLEKRTISPDNCITQLFFLHLPACAEIFLLIIVADRYV 124
Db 71 NLSLEIGYTCVSIPKMLQSLVSEARGISWEGASQMFPIFGITCCCLAAVAFPRYM 130
Qy 125 AICTPLHYPNVMNRVCIOVFLMWGLGTVHSLGQTFLLTRLPYCGPNIIDSFCVPLV 184
Db 131 AICSPHLYATRMRSRGVCAIYAIWSWGCIVGLQTNFISLNCPCGEIDHFFCDLPPL 190
Qy 185 IKLACTDTYLLGLIVNSGRTISLSCFLAVTSYMWILVS-LRGSAREGROKALSTCSAH 243
Db 191 LALACGTSIQNEALIFAAVLCITSPFLIISIVRILVAVLVMPSPBGRKALSTCSSH 250
Qy 244 FMVVALFFGPCIFLYTRPDTSFS--IDKVVSVFYTVVTPPLNPFITLRNEEVSAMKO 300
Db 251 LHVTLTFYGSATSYATLSSKSHSPGVKDLALFTYTSVMNLPIIYSLRNKEVVGALRR 309

RESULT 11
US-08-748-506-13

; Sequence 13, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-748-506-13

Query Match 38.3%; Score 617.5; DB 3; Length 321;
Best Local Similarity 42.0%; Pred. No. 9.3e-45;
Matches 129; Conservative 59; Mismatches 102; Indels 17; Gaps 4;
Qy 5 NOTRTEFVFLGLDNRVLEMLPFMAFSAIYMLTSGNIIIIITVFTPSLHTPMYFELS 64
Db 11 NSLSVKRFAPAKSEVGECEFLFTLLILMFVSLTGNLIALAICTSPSLHTPMYFELA 70
Qy 65 NLSFDICHSSVTPPKMLEGLLEKRTISPDNCITQLFFLHLPACAEIFLLIIVADRYV 124
Db 71 NLSLEIGYTCVSIPKMLQSLVSEAREIFQVGCATQMFPIFGITCCCLAAVAFPRYM 130
Qy 125 AICTPLHYPNVMNRVCIOVFLMWGLGTVHSLGQTFLLTRLPYCGPNIIDSFCVPLV 184
Db 131 AICSPHLYATRMRSRGVCAIYAIWSWGCIVGLQTNFISLNCPCGEIDHFFCDLPPL 190
Qy 185 IKLACTDT-----VLTGLIVNSGRTISLSCFLAVTSYMWILVS-LRKSAREGROK 236
Db 191 LALACGTSIQNEAIVVVVLCIS-----SPFLIISIVRILVAVLVMPSPBGRKAL 243
Qy 237 LSTCSAHFMVVALFFGPCIFLYTRPDTSFS--IDKVVSVFYTVVTPPLNPFITLRNEE 294
Db 244 LSTCSSHLVLTFLYSGSVTYLRPFSKSHSPGMDKLLALFYRAVTSMLNPIIYSLRNKV 303
Qy 295 KSAMKQ 301
Db 304 KAALRR 310

RESULT 12
US-08-118-270-61
; Sequence 61, Application US/08118270
; Patent No. 5508384

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GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-61

Query Match      37.2%; Score 599.5; DB 1; Length 284;
Best Local Similarity 41.9%; Pred. No. 2.7e-43;
Matches 117; Conservative 61; Mismatches 94; Indels 7; Gaps 4;

QY 26 LFFMAFSATYMLTSLGNIILIIATVFTPSLHTPMYFFLSNLSFIDICHSSVTPKXLEGI 85
DB 1 LFLFLIMLYATLVAGNLIILAIIGDSSLHTPMYFFLSNLSFVDCFSSTVPKXLANH 60
QY 86 LERKTIISPDNCITQLFHLFACAEIFLLIIIVADRYVAICTPLHYPNMNRVCIOY 145
DB 61 ILGSAISFSGCLTQLYFLAVFGNMDNFLAVMSYDRVAICHPLHTTI--ROLCVLLV 118
QY 146 PALMIGCTVHSGQTFRLTRLPYCGPNIIIDSYCDVPLVIKACTDVTYLTGILIVTNSGT 205
DB 119 VGSVAVANNNCGLHLILIMARKSFCD--LPHFCDGTPLKLSGSDTHNELMILTEGAV 176
QY 206 ISLSCFLAVTISYMWILVS-LRKHSABGRQKALSTCSAHFMVVALFPGPCIFITYRPTDS 264
DB 177 VWATFVCLISIIYHITCAVLKRVSSPRGGKMSFTGSHIAVCLFYGTIVAVENPSSS 236
QY 265 F--SIDKVVSVFYTVTPLNPIYTLRNEEVKSANKOL 301
DB 237 HLAGRDMAAAVMYAVVTPEINPIYSLRNSDKKALRKV 275

RESULT 13
PCT-US93-08528-61
Sequence 61, Application PC/TUS93308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

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NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-61

Query Match      37.2%; Score 599.5; DB 5; Length 284;
Best Local Similarity 41.9%; Pred. No. 2.7e-43;
Matches 117; Conservative 61; Mismatches 94; Indels 7; Gaps 4;

QY 26 LFFMAFSATYMLTSLGNIILIIATVFTPSLHTPMYFFLSNLSFIDICHSSVTPKXLEGI 85
DB 1 LFLFLIMLYATLVAGNLIILAIIGDSSLHTPMYFFLSNLSFVDCFSSTVPKXLANH 60
QY 86 LERKTIISPDNCITQLFHLFACAEIFLLIIIVADRYVAICTPLHYPNMNRVCIOY 145
DB 61 ILGSAISFSGCLTQLYFLAVFGNMDNFLAVMSYDRVAICHPLHTTI--ROLCVLLV 118
QY 146 PALMIGCTVHSGQTFRLTRLPYCGPNIIIDSYCDVPLVIKACTDVTYLTGILIVTNSGT 205
DB 119 VGSVAVANNNCGLHLILIMARKSFCD--LPHFCDGTPLKLSGSDTHNELMILTEGAV 176
QY 206 ISLSCFLAVTISYMWILVS-LRKHSABGRQKALSTCSAHFMVVALFPGPCIFITYRPTDS 264
DB 177 VWATFVCLISIIYHITCAVLKRVSSPRGGKMSFTGSHIAVCLFYGTIVAVENPSSS 236
QY 265 F--SIDKVVSVFYTVTPLNPIYTLRNEEVKSANKOL 301
DB 237 HLAGRDMAAAVMYAVVTPEINPIYSLRNSDKKALRKV 275

RESULT 14
US-08-118-270-60
Sequence 60, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK

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